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- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

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STIC-Biotech/ChemLib

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Sent	:

Kaushal, Sumesh

Wednesday, June 11, 2003 2:59 PM STIC-Biotech/ChemLib

To: Subject:

09/663542: SEQ search

09/663542: SEQ search

Title: PHOSPHODIESTERASE ENZYMES

Inventor: FIDOCK, MARK

Please search

SEQ ID NO:1

SEQ ID NO:1 1-194

SEQ ID NO:2

priority: 01/21/00

thanks

S. Kaushal

CM1 12A07 AU1636 Ph: 703-305-6838

Mail Box: 11E12

Searcher:	
Phone:	
Location:	
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Clerical:	
Online time:	

TYPE OF SEARCH:	1
NA Sequences:	<u> </u>
AA Sequences:	2
Structures:	
Bibliographic:	
Litigation:	
Full text:	
Patent Family:	
Other:	

VENDOR/COST (where applic.) STN: DIALOG: Questel/Orbit:_ DRLink:_ Lexis/Nexis:_ Sequence Sys.: 1 WWW/Internet:_ Other (specify):

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File: 09663542

IDS
SEQ Search -- Interference Search Removed [X] 6/28/03
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Notes:

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Run on:

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Result М О Searched:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific TITLE OF INVENTION: Phosphodiesterase Materials and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Marshall, O'Toole, Gerstein, Murray & 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,547A
           US-08-455-526-45
US-08-455-526-45
US-08-455-526-45
US-09-139-491-39
US-08-297-444-39
US-08-297-510-39
US-08-479-532-39
US-08-455-526-39
US-08-455-526-39
US-09-78-72-644-43
US-09-78-72-644-43
US-08-297-494-43
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APPLICANT: Corbin, Jackie D.
APPLICANT: Ferguson, Kenneth M.
APPLICANT: Francis, Sharron H.
APPLICANT: Kadlecek, Ann
APPLICANT: Loughney, Kate
APPLICANT: McAllister-Lucas, Linda M.
APPLICANT: Sonnenburg, William K.
APPLICANT: Thomas, Melissa K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/08480547A Patent No. 5652131 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION. TO ATTORNEY ATTORNEY AGENT INFORMATION:
NAME: No. 5652131and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFA: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 10:
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amino acid
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CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein US-08-480-547A-10
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COUNTRY: USA
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FILING DATE:
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Sequence 23,
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                                                                                                         June 13, 2003, 15:46:07; Search time 5.52392 Seconds
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.: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
?: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
?: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
!: /cgn2_6/ptodata/1/iaa/6COMB.pep:*
?: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
>: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
           version 5.1.6
- 2003 Compugen Ltd.
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US-08-250-847B-10
US-08-463-949A-10
US-08-463-949A-10
US-08-464-410A-10
US-08-464-410A-23
US-09-226-741-5
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US-09-226-741-3
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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McAllister-Lucas, Linda M.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/068,051
                                                                                                                                                                                          ; Sequence 10, Application US/08250847B; Patent No. 5702936; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      Sonnenburg, William K.
Thomas, Melissa K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                               Beavo, Joseph A.
Corbin, Jackie D.
Ferguson, Kenneth M.
Francis, Sharron H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 10:
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US
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                                                                      173 CSVLLLED 180
                                                                                                367 CTIFIVDE 374
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
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Best Local Similarity
Matches 59; Conserv
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APPLICANT:
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                                                                    54 KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAIN-KIPEGAPFTEDDEKVMQMY 112
                                                                                                                     113 LPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCER 172
                                                                                                                                         1; Gaps
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APPLICANT: McAllister-Lucas, Linda M.
APPLICANT: Sonnenburg, William K.
APPLICANT: Thomas Unitsas K.
TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific TITLE OF INVENTION: Phosphodiesterase Materials and Methods
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive CITY: Chicago STATE: Illinois COUNTRY: USA
46.1%; Pred. No. 3.1e-26;
Live 31; Mismatches 37; Indels
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46.1%; Pred. No. 3.1e-26;
tive 31; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/480,547A
                                                                                                                                                                                                                                                                                                                Sequence 23, Application US/08480547A Patent No. 5652131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: No. 5652131and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32791
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     Corbin, Jackie D.
Ferguson, Kenneth M.
Francis, Sharron H.
Kadlecek, Ann
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                     Beavo, Joseph A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 875 amino acids
amino acid
Best Local Similarity 46.1
Matches 59; Conservative
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                                                                                                                                                                                            173 CSVLLLED 180
                                                                                                                                                                                                                     357 CTIFIVDE 364
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59; Conserva
                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90909
                                                                                                                                                                                                                                                                              RESULT 2
US-08-480-547A-23
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54 KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAIN-KIPEGAPFTEDDEKVMQMY 112
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EDPRENAEVDQITGYKTQSILCMPIKNHREEVVGVAQAINKKSGNGGTFTEKDEKDFAAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific TITLE OF INVENTION: Phosphodiesterase Materials and Methods NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: Marshall, O'Toole, Gerstein, Murray & Borun
6300 Sears Tower, 233 S. Wacker Drive
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Pred. No. 3.1e-26;
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                          APPLICANT: Sonnenburg, William K.
APPLICANT: Thomas, Melissa K.
TITLE OF INVENTION: Cyclic GMP-Specific
TITLE OF INVENTION: Phosphodiesterase Materials and Methods
                                                                                                                                                                                                                                                                                                                                                                           E: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 S. Wacker Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.5%; Score 307.5; DB 1
llarity 46.1%; Pred. No. 3.1e-26;
Conservative 31; Mismatches 37
                                                                                                                                                                                                                              Kadlecek, Ann
Loughney, Kate
McAllister-Lucas, Linda M.
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APPLICATION NUMBER: US 08/068,051
FILING DATE: 27-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                             Sequence 23, Application US/08250847B Patent No. 5702936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No. 5702936and, Greta E. RATION NUMBER: 35,302 NCE/DOCKET NUMBER: 32083
                                                                                                                                                                            Corbin, Jackie D.
Ferguson, Kenneth M.
Francis, Sharron H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
LENGTH: 875 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION
                                                                                                                                                                Beavo, Joseph A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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CLASSIFICATION: 435
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367 CTIFIVDE 374
173 CSVLLLED 180
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357 CTIFIVDE 364
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Best Local Similarity
Matches 59; Conserv
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STATE: Illinois
                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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APPLICANT:
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54 KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAIN-KIPEGAPFTEDDEKVMQMY 112
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                                                                                                                                                                                                                                APPLICANT: Thomas, Melissa K.
TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
TITLE OF INVENTION: Phosphodiesterase Materials and Methods
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,949A
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46.1%; Pred. No. 3.1e-26;
tive 31; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/068,051
FILING DATE: 27-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5955583and, Greta E.
REGISTRATION NUMBER: 35,3022
                                                                                                                                                                                        McAllister-Lucas, Linda M.
Sonnenburg, William K.
Thomas, Melissa K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Sequence 10, Application US/08463949A Patent No. 5955583
                                                                                 Corbin, Jackie D.
Ferguson, Kenneth M.
Francis, Sharron H.
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                                                                                                                                                                         Loughney, Kate
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Best Local Similarity 46.1%
                                                                                                                                                 Kadlecek, Ann
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                         GENERAL INFORMATION: APPLICANT: Beavo,
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US-08-463-949A-23
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Francis, Sharron H.
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357 CTIFIVDE 364
                                                                                                                                            NUMBER OF SEQUENCES:
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Best Local Similarity
Matches 59; Conserv
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STATE: Illinois
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US-08-464-410A-23
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                                                     APPLICANT:
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                                                                                                    APPLICANT: McAllister-Lucas, Linda M.
APPLICANT: Sonnerburg, William K.
APPLICANT: Thomas, Melissa K.
APPLICANTION: Cyclic GMP-Binding, Cyclic GMP-Specific TITLE OF INVENTION: Phosphodiesterase Materials and Methods NUMBER OF SEQUENCES: 23
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6300 Sears Tower, 233 S. Wacker Drive
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46.1%; Pred. No. 3.1e-26;
tive 31; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.25
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PRIOR APPLICATION DATA.

APPLICATION NUMBER: US 08/068,051

FILING DATE: 27-MAY-1993

ATOKNEY AGENT INFORMATION:
NAME: NO. 595583and, Greta E.
REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 32706

TELECOMMUNICATION INFORMATION:
TELEFAN: (312) 474-6300

TELEFAN: (312) 474-6300

TELEFAN: 25-3856

INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,949A
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentr P.'
                                                  Ferguson, Kenneth M.
Francis, Sharron H.
Kadlecek, Ann
Loughney, Kate
              Beavo, Joseph A.
Corbin, Jackie D.
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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Matches 59; Conserva
                                                                                                                                                                                                                                                                                  Chicago : Illinois
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-463-949A-23
                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                    APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                    CITY: C
                                                  APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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US-08-464-410A-10; Sequence 10, Application US/08464410A; Patent No. 6037119; GENERAL INFORMATION:

Beavo, Joseph A. Corbin, Jackie D.

APPLICANT: APPLICANT:

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113 LPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCER 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAIN-KIPEGAPFTEDDEKVMQMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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; Pred. No. 3.1e-26;
31; Mismatches 37; Indels 1:
                                                               APPLICANT: Sonnenburg, William K.
APPLICANT: Thomas, Melissa K.
TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
TITLE OF INVENTION: Phosphodiesterase Materials and Methods
                                                                                                                                                                                                    E: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,410A
FILING DATE: Une 5, 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALTERENT SERVITOR STATES TO SERVITOR STATES TO SET SECURITION NUMBER: 35,302

REGISTRATION NUMBER: 35,302

REFERENCE/POCKET NUMBER: 27866/32705

TELEPHONE: (312) 474-6300

TELEPHONE: (312) 474-6400

TELEPHONE: (312) 474-0448

TELERS: 25-3856

INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kadlecek, Ann
Loughney, Kate
McAllister-Lucas, Linda M.
Sonnenburg, William K.
Thomas, Mellissa K.
                                            McAllister-Lucas, Linda M.
                                                                                                                                                                                                                                                                                                                                                                                                                  PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 23, Application US/08464410A
Patent No. 6037119
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corbin, Jackie D.
Ferguson, Kenneth M.
Francis, Sharron H.
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31.58;
46.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beavo, Joseph A.
Kadlecek, Ann
Loughney, Kate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             875 amino acids amino acids
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LENGTH: 875 amino acid
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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54 KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAIN-KIPEGAPFTEDDEKVMQMY 112
                                                                                                                                                                                    113 LPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCER 172
                                                                                                                                                                                                           113 LPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCER 172
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; Sequence 23, Application PC/TUS9406066
; GENERAL INFORMATION:
APPLICANT: The Board of Regents of the University of Washington
; TITLE OF INVENTION:
TITLE OF INVENTION: Phosphodiesterase Materials and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 875;
                                      Length 875;
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                                                                            Indels
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                                      DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31.5%; Score 307.5; DB 4;
nilarity 46.1%; Pred. No. 3.1e-26;
Conservative 31; Mismatches 37;
                                                                            37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lanfear, Jerry
APPLICANT: Fawcett, Lindsay
APPLICANT: Bandman, Olga
TITLE OF INVENTION: HUMAN CYCLIC NUCLEOTIDE PDES
FILE REFERENCE: PF-0623-1 CIP
                                      Score 307.5; DB 3
Pred. No. 3.1e-26;
1; Mismatches 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/595,514
CURRENT FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: 09/226,741
PRIOR FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/09595514 Patent No. 6416991
                                                                         31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phillips, Stephen C.
                                        31.5%;
46.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: GI 3355606
US-09-595-514-5
                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CSVLLLED 180
                                                                                                                                                                                                                                                                                    |::::::
CTIFIVDE 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTIFIVDE 374
                                                                                                                                                                                                                                                             173 CSVLLLED 180
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Best Local Similarity
The 59; Conserva
                                        Query Match
Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Phillips
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                                                                                                                                                                                                                                                                                                                                                                         US-09-595-514-5
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   US-09-226-741-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 LPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCER 172
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   Cyclic GMP-Binding, Cyclic GMP-Specific
Phosphodiesterase Materials and Methods
                 STREET: 6300 Sears Tower, 233 S. Wacker Drive STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                            COPERATING SYSTEM: PC-DORAGIBLE OVERTHING SYSTEM: PC-DOS/MS-DOS SOFWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,410A FILING DATE: June 5, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09226741
Patent NO. 6100037
GENERAL INFORMATION:
APPLICANT: Phillips, Stephen C.
APPLICANT: Lanfear, Jerry
APPLICANT: Bancett, Lindsay
APPLICANT: Bancett, Lindsay
APPLICANT: Bandman, Olga
TITLE OF INVENTION: HUMAN CYCLIC NUCLEOTIDE PDES
FILLE REFERENCE: PF-0623 US
CURRENT APPLICATION NUMBER: US/09/226,741
CURRENT FILING DATE: 1999-01-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31.5%; Score 307.5; DB 3; 46.1%; Pred. No. 3.1e-26; tive 31; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                             27866/32705
                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: NO. 6037119and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE: OTHER INFORMATION: GI 3355606
                                                                                                                                                                                                                                                                                                                                                                                                                                                : (312) 474-6300
(312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            875 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 46.19
Matches 59; Conservative
TITLE OF INVENTION: Cycl
TITLE OF INVENTION: Phos
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: HOMO SAPIENS
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367 CTIFIVDE 374
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LENGTH: 875
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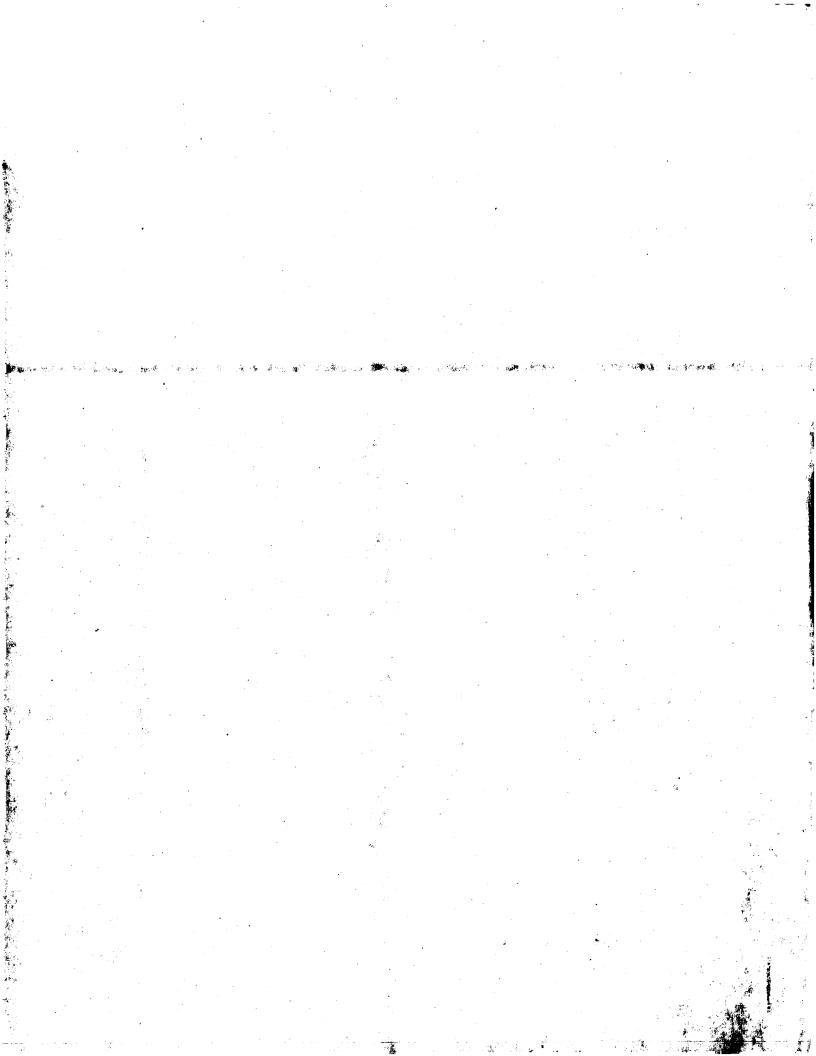
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72 PIWNSNHQIIGVAQVLNRL-DGKPFDDADQRLFEAFVIFCGLGINNTIMYDQVKKSWAKQ 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 LPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCER 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 PIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYLPFCGIAISNAQLFAASRKEYERS 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 SLAEKQEK--HQDFLIQRQTKT------KDRRFNDEIDKLTGYKTKSLLCM
                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                              Length 875;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Phillips, Stephen C.
APPLICANT: Phillips, Stephen C.
APPLICANT: Lanfear, Jerry
APPLICANT: Bawcett, Lindsay
APPLICANT: Bandman, Olga
TITLE OF INVENTION: HUMAN CYCLIC NUCLEOTIDE PDES
FILE REFERENCE: PF-0623 US
CURRENT APPLICATION NUMBER: US/09/226,741
CURRENT FILLING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3.3
LENGTH: 367
                                                                                                                                                                                                                                                                                                                                                                                                  DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 19.1%; Score 186; DB 3; Best Local Similarity 29.7%; Pred. No. 6.1e-13; Matches 38; Conservative 35; Mismatches 37
                                                                                                                                                                                                                                                                                                                                                                                              Query Match 30.9%; Score 301.5; DB 5
Best Local Similarity 45.3%; Pred. No. 1.5e-25;
Matches 58; Conservative 32; Mismatches 37
                       US 08/068,051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09226741 Patent No. 6100037
                                                                                 NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 320
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                  TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 10:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06
FILING DATE: 27-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTHER INFORMATION: HSPDE10A2 US-09-226-741-3
                                                                                                                                                                                                                                                                      : 875 amino acids
amino acid
                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                              ) MOLECULE TYPE: protein PCT-US94-06066-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 CSVLLLED 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTIFIVDE 364
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                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 LPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCER 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: The Board of Regents of the University of Washington TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific TITLE OF INVENTION: Phosphodiesterase Materials and Methods NUMBER OF SEQUENCES: 23 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2IP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible.
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.5%; Score 307.5; DB 5 46.1%; Pred. No. 3.1e-26; tive 31; Mismatches 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US94/06066 FILING DATE:
                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/068,051
FILING DATE: 27-WAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application PC/TUS9406066 GENERAL INFORMATION:
                                                                                 'E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233
                                                                                                                                                                                                                                                                                                                                                      35,302
                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 875 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                NAME: Noland, Greta E. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 46.1
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTIFIVDE 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173 CSVLLLED 180
                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Chicago
STATE: Illinois
COUNTRY: USA
    Illinois
                                                                                                                                                                                                                              CLASSIFICATION:
                       USA
                                                                                                                                                                                                        FILING DATE:
                                        90909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT-US94-06066-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                   COUNTRY:
  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---KDRRFNDEIDKLTGYKTKSLLCM 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 SFKESSMEKSSYSDWLINNSIAELVASTGLPVNISDAYQDPRFDAEADQISGFHIRSVLCV 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
19.1%; Score 186; DB 3; Length 490;
Best Local Similarity 29.7%; Pred. No. 9.3e-13;
Matches 38; .Conservative 35; Mismatches 37; Indels 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 29.7%; Pred. No. 6.1e-13;
Matches 38; Conservative 35; Mismatches 37; Indels
                                                                                                                                                                        APPLICANT: Phillips, Stephen C.
APPLICANT: Phillips, Stephen C.
APPLICANT: Landear, Jerry
APPLICANT: Bandean, Olga
TITLE OF INVENTION: HUMAN CYCLIC NUCLEOTIDE PDES
FILE REFERENCE: PF-0623-1 CIP
CURRENT FILING DATE: 2000-06-14
PRIOR FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8: SEQ ID NOS: 7
LENGTH: 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Phillips, Stephen C.
APPLICANT: Lanfear, Jerry
APPLICANT: Fawcett, Lindsay
APPLICANT: Famoman, Olga
TITLE OF INVENTYON: HUMAN CYCLIC NUCLEOTIDE PDES
FILE REFERENCE: PF-0623 US
CURRENT APPLICATION NUMBER: US/09/226,741
CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 SLAEKQEK--HQDFLIQRQTKT-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-226-741-1; Sequence 1, Application US/09226741; Patent No. 6100037; GENERAL INFORMATION:
                                                                                                                Sequence 3, Application US/09595514 Patent No. 6416991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: HOMO SAPIENS
COTHER INFORMATION: HSPDE10A2
US-09-595-514-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: HSPDE10A1
US-09-226-741-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: HOMO SAPIENS
|:|::
131 SVALDVLS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 RALLEVVN 144
                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Phillip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 1
LENGTH: 490
                                                                            RESULT 14
US-09-595-514-3
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34 SLAEKQEK--HQDFLIQRQTKT------KDRRFNDEIDKLTGYKTKSLLCM 76

οy



- protein search, using sw model OM protein

June 13, 2003, 15:45:35 ; Search time 7.51253 Seconds Run on:

(without alignments) 2482.530 Million cell updates/sec

US-09-663-542-1_COPY_1_194 975 1 MLKQARRPLFRNVLSATQWK......VLLLEDIESPVVKFTKSFEL 194 score: Title: Perfect so Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 Total number of hits satisfying chosen parameters:

283224 segs, 96134422 residues

Searched:

length: 0 length: 2000000000 sed 0B Minimum I Maximum I

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* PIR_73:* Database :

Pred. No. is the number of results predicted by chance to have a . score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	-cvclic-	ပ်	'-cyclic-	',5'-cyclic-	',5'-cyclic-	',5'-cyclic-	'-cyclic-	,5	',5'-cyclic-	•	ypothetical			n)	adenylate cyclase	3',5'-cyclic-GMP p	-cyclic-nucl	S	two-component sens	GAF domain protein	serine/threonine k	serine/threonine k			protein R08D7.6 [i		hypothetical prote		hypothetical prote
н	JW0106	_	ന	3	\sim	コ	B34611	A47451	A42828	S13030	T25590	S13032	S30762	AB2044	AC2089	A36617	JC2486	A40981	AC2073	·D71613	AC1917	AG2391	g	S24462	D88544	AB1847	E70645	C208	4.1
Length DB	75	75	52	55	28	59	59	856 1	54	59	93	00	26	09	29	23	28	21	44	245	20	006	73	41	18	80	78	77	49
% Query Match		Н	Ч	0	20.0	σ	19.4	19.1	ω.	•	ъ.	•		ω.	7.	7		15.8	•	12.2		Ξ.			10.3	φ.	•	٠	٠
Score	307.5	307.5	205.5	195	195	193	189	186	183	183	180.5	180	180	178.5	174.5	170	159	154	129	118.5	118.5	116	111.5	100	100	95	94.5	94	92.5
Result No.	!	7	m	4	Ŋ	9	7	80	o	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

probable U5 snRNP-	hypothetical prote	two-component sens	IAP100 protein (im	serine/threonine k	serine/threonine k	serine/threonine k	hypothetical prote	hypothetical prote	myosin heavy chain	mysoin heavy chain	mysoin heavy chain	acetyl-CoA carboxy	IMP dehydrogenase	rhoptry protein -	NAM-like protein -
T39188	B83899	H83716	F90106	AC1895	AD1895	AD2267	H84013	F72363	A53016	B59254	A59254	S60200	G64501	T28676	T49054
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2176 2	735	502	1070	1796	1799	2021	515	758	812	1828	1855	2185	496	2401	319
				9.1 1796											
9.4	9.4		9.3	9.1		9.1		8.9		6.8	6.8	6.8		8.8	

ALIGNMENTS

		Lerase (EC 3.1.4.3
		phosphodiesterase
SULT 1	10106	,5'-cyclic-GMP

RESULT 1

Widnows

J, 5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) 5A - human

N.Alternate names: PDE5A1

C; Species: Homo sapiens (man)

C; Species: Homo sapiens (man)

C; Species: Homo sapiens (man)

C; Stacey, P.; Rulten, S.; Dapling, A.; Phillips, S.C.

Biochem: Looping and expression of human cGMP-binding cGMP-specific phospho

A; Reference number: JW0106, MUID: 98308101; PMID: 9642111

A; Residues: 1-875 cSTA>

A; Residues: 1-875 cSTA>

A; Cross-references: GB:AJ004865; NID: 93355605; PIDN: CAA06170.1; PID: 93355606

C; Genetics: A; Cross-references: GB:AJ004865; NID: 93355605; PIDN: CAA06170.1; PID: 93355606

C; Genetics: A; Cross-references: GB:AJ004865; NID: 93355605; PIDN: CAA06170.1; PID: 93355606

C; Genetics: A; Cross-references: GB:AJ004865; NID: 93355605; PIDN: CAA06170.1; PID: 93355606

C; Genetics: A; Cross-references: GB:AJ004865; NID: 93355605; PIDN: CAA06170.1; PID: 93355606

C; Genetics: A; Cross-references: GB:AJ004865; NID: 93355605; PIDN: CAA06170.1; PID: 93355606

C; Genetics: A; Cross-references: GB:AJ004865; NID: 93355605; PIDN: CAA06170.1; PID: 93355606

C; Genetics: A; Cross-references: GB:AJ004865; NID: 93355605; PIDN: CAA06170.1; PID: 93355606

C; Genetics: A; Cross-references: GB:AJ004865; NID: 93355605; PIDN: CAA06170.1; PID: 93355606

C; Genetics: A; Cross-references: GB:AJ004865; NID: 93355605; PIDN: CAA06170.1; PID: 93355606

C; Superfamily: 3',5'-cyclic-GMP phosphodiesterase Amonlogy CNND>

C; Reywords: alternative splicing: CGMP binding; Phosphodiesterase Amonlogy CNND>

F; 612-835/Domain: 3',5'-cyclic-nucleotide phosphodiesterase Amonlogy Ristaus pre

F; 102/Binding site: Phosphate (Ser) (covalent) (by cGMP-dependent kinase) #status pre

Gaps 7; DB 1; Length 875; Query Match 31.5%; Score 307.5; DB 1; Length EBest Local Similarity 46.1%; Pred. No. 3.4e-17; Matches 59; Conservative 31; Mismatches 37; Indels

54 KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAIN-KIPEGAPFTEDDEKVMQMY 112 δ

306 qq

113 LPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCER 172 δŏ

QQ

173 CSVLLLED 180 οy

1:: :::: 367 CTIFIVDE 374

QQ

3,'5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) 5A - bovine
3,'5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) 5A - bovine
N'Alternate names: PDE5A1
C'Species: Bos primigenius taurus (cattle)
C'Spec

10:15:15

23

Jun

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C; Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                         A; Status: preliminary A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S63688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213
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150186
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) - chicken
C;Species: Gallus gallus (chicken)
C;Decies: Gallus gallus (chicken)
C;Decies: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000
C;Accession: 150186
R;Semple-Rowland, S.L.; Green, D.A.
Exp. Eye Res. 59, 365-372, 1994
A;Title: Molecular characterization of the alpha'-subunit of cone photoreceptor cGMP phota; Exp. Eye Res. 59, 365-372, 1994
A;Title: Molecular characterization of the By MID: 7821382
A;Accession: 150186
A;Accession: 150186
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-862 <SEM>
A;Residues: 1-862 <SEM>
A;Cross-references: GBBL129233; NID: 9495742; PIDN: AAC42223.1; PID: 9495743
C;Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
F;561-794/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
A; Molecule type: mRNA
A; Residues: 1-875 <MCAN.
A; Cross-references: GB:L16545
A; Experimental source: lung
R; Thomas, M.K.; Francis, S.H.; Corbin, J.D.
A; Biol. Chem. 255, 14971-14978, 1990
A; Title: Substrate- and kinase-directed regulation of phosphorylation of a cGMP-binding
A; Reference number: A35807
A; Reference number: A35807
A; Molecule type: protein
A; Residues: 90-101 <FHO>
C; Superfamily: 3', 5' cyclic-GMP phosphodiesterase 5A; 3', 5' cyclic-nucleotide phosphodic
C; Superfamily: 3', 5' cyclic-nucleotide phosphodiesterase homology <CRPD>
C; Keyworts: alternative splicing; cGMP binding; phosphorotein: phosphoric diester hydre
F; 602-825, Domain: 3', 5' -cyclic-nucleotide phosphodiesterase homology <CRPD>
F; 92/Binding site: phosphate (Ser) (covalent) (by cGMP-dependent kinase) #status predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 LPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCER 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYLPFCGIA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | :|| ||| | ::: :|| : | :: | | :|| DYLDKKTGYTTVNMMAIPI-TQGKEVLAVVMALNKL-NASEFSKEDEEVFKKYLNFISLV 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 TRLLNVTPTS-----KFEDNLVNPDKETVFPLDIGIAGWVAHTKKFFNIPDVKKNNHFS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 ISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCERCSVLLLE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A34810
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) alpha' chain, cone - bovine
C:Species: Bos primigenius tauruș (cattle)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAIN-KIPEGAPFTEDDEKVMQMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                            Length 875;
                                                                                                                                                                                                                                                                                                                                                                                                    31.5%; Score 307.5; DB 1; Lenyun 46.1%; Pred. No. 3.4e-17; uismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 205.5; DB 2
Pred. No. 6.7e-09;
4; Mismatches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34;
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29.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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CTIFIVDE 364
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59; Conserv
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Best Local 8
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A; Molecule type: mRNÅ
A; Residues: 308-502 < CHA>
A; Residues: 308-502 < CHA>
A; Crass references: GB:M33140; NID:g163492; PIDN:AAA30688.1; PID:g163493; GB:M29465
A; Note: parts of this sequence were confirmed by protein sequencing
C; Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotid
C; Keywords: cGMP binding; phosphoric diester hydrolase
E; 556-789/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Introns: 160/5; 211/3; 241/3; 288/3; 313/3; 335/2; 357/3; 373/3; 423/3; 471/3; 494/
C; Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotid
C; Keywords: GGMP binding: lipoprotein; phosphoric diester hydrolase; photoreceptor; p
F; 560-770/Domain: actalytic #status predicted <CATP.
F; 561-794/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>
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R; Feshchenko, E.A.; Andreeva, S.G.; Suslova, V.A.; Smirnova, E.V.; Zagranichny, V.E.; FEBS Lett. 381, 149-152, 1996
A; Title: Human cone-specific CGMP phosphodiesterase alpha' subunit: complete cDNA seq A; Reference number: S63688; MUID:96193933; PMID:8641425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-115, 'V', 117-269, 'S', 271-372, 'P', 374-463,'L', 465-564,'Q', 566-858 <VIC>
A; Cross-references: GB:U31973: NID:9540230; PIDN:AAA96392.1; PID:9940231
A; Note: this sequence lacks a residue Tyr after the 231-Met, and has an additional re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a cDNA encoding the alpha' subunit of huma
PMID:8543163
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P.J.; Wals
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A; Residues: 1.858 cFES>
A; Cross-references: EMBL:X94354; NID:g1616594; PIDN:CAA64079.1; PID:g1149517
A; Note: intron positions were determined by partial sequencing of genomic DNA
R; Viczian, A.S.; Piriev, N.I.; Farber, D.B.
Gene 166, 205-211, 1995
A; Title: Isolation and characterization of a cDNA encoding the alpha' subunit
A; Reference number: JC4520; MUID:96125191; PMID:8543163
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C;Date: 08-Feb-1996 #sequence_revision 11-Apr-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYL
                                                                                                                                                                                                                                                                                           A; Residues: 1.855 - LITS A; CLITS A; CLITS A; CLITS B; CLITS B; CLITS B; CLITS B; Charbonneau, H; Prüsti, R.K.; Lefrong, H; Sonnenburg, W.K.; Mullaney, Proc. Natl. Acad. Sci. U.S.A. 87, 288-292, 1990 A; Title: Identification of a noncatalytic cGMP-binding domain conserved in A; Reference number: A34809; MUID:90115859; PMID:2153290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ,5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) alpha' chain - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.0%; Score 195; DB 2; 36.5%; Pred. No. 4.8e-08;
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3.7.5.-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta chain - dog C; Species: Canis lupus familiaris (dog)
C; Species: Canis lupus familiaris (dog)
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jan-2000
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jan-2000
C; Accession: A47451; S34290
R; Suber, M.L.: Pittler, S.J.: Qin, N.; Wright, G.C.; Holcombe, V.; Lee, R.H.; Craft, Proc. Natl. Acad. Sci. U.S.A. 90, 3968-3972, 1993
A; Title: Irish setter dogs affected with rod/cone dysplasia contain a nonsense mutatine A; Reference number: A47451; MUID:93248211; PMID:8387203
A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
A; Residues: 1-856 <SUB>
A; Cross-references: GB:Z23014; NID:g31237
A; Experimental source: Irish setter, retina
A; Note: sequence inconsistent with the nucleotide translation
A; Note: sequence extracted from NCBI backbone (NCBIN:130783)
R; Clements, P.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GDB:120265; OMIM:180071
A; Map position: 5q31.2-5q34
C; Superfamily: 3',5'-cyclic-cAPP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotid C; Superfamily: 3',5'-cyclic-nucleotid C; Sewords: cGMP binding: phosphoric diester hydrolase F;558-791/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 21-Jan-2000
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 21-Jan-2000
C;Accession: B34611
R;Pittler, S.J; Baehr, W.; Wasmuth, J.J.; McConnell, D.G.; Champagne, M.S.; vanTuine Genomics 6, 272-283, 1990
A;Titler, Molecular characterization of human and bovine rod photoreceptor cGMP phosph A;Reference number: A34611; MUID:90169986; PMID:2155175
A;Accession: B34611
    114 PFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC 173
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3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) alpha chain - human
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A;Reference number: S34290
A;Accession: S34290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-859 <PIT>
A;Cross-references: GB:M26061
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVLLLE 179
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Best Local Similarity
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                                                                                                                                                                          174
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SIGNATE

3.7.5 - CYCILC-GMP phosphodiesterase (EC 3.1.4.35) alpha chain - bovine

NALetratae names: GGMP phosphodiesterase (EC 3.1.4.35) alpha chain

C. Species: Sep Finityaenis: Laturs: GCATLD:

T. M.: Species: Sep Finityaenis: Laturs: GCATLD:

R. Wohlminkov, Y. A.: GLabanov, V. V.; Lipkin, V. W.

T. M.: Species: Sep Finityaenis: Laturs: GCATLD:

A. Reference number: SGA18

A. Reference number: SGA18

A. Rocession: Robert A. A. SGA18

A. Rocession: SGA18

A. Rocession: Robert A. A. SGA18

A. Rocession: Robert A. A. SGA18

A. Rocession: Robert A. A. SGA18

A. Rocession: SGA18

A. Rocession: SGA18

A. Rocession: Robert A. A. SGA18

A. Rocession: Robert A. A. SGA18

A. Rocession: Robert A. A. SGA19

A. Robert A. Robert A. A. SGA19

A. Robert A. Robert A. A. SGA19

A. Robert A. Robert A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       114 PFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC 173
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                                                                                                                                                                                                                                                                                                               Gaps
F;855/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52; Indels
                                                                                                                                                                     54; Indels
                                                                                            Length
                                                                                  Query Match
20.0%; Score 195; DB 2;
Best Local Similarity 37.3%; Pred. No. 4.8e-08;
Matches 47; Conservative 23; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.8%; Score 193; DB 1;
ilarity 34.1%; Pred. No. 7e-08;
Conservative 29; Mismatches E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVLLLE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGLLD 283
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Best Local Similarity
Matches 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174
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A Molecule type: DNA
A; Residues: 1-859 <RAD>
A; Residues: 1-859 <RAD>
A; Cross-references: EMBL:X60664; NID:953587; PIDN:CAA43072.1; PID:953588
C; Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotid
C; Keywords: CGMP binding: phosphoric diester hydrolase
F; 558-791/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: $13030
R; Baehr, W.; Champagne, M.S.; Lee, A.K.; Pittler, S.J.
FEBS Lett. 278, 107-114, 1991
A; Title: Complete CDNA sequences of mouse rod photoreceptor cGMP phosphodiesterase alcing of the beta-subunit gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 : 1 | 1 : 1 | 1 : 1 | 215 | 216 NFVNLIMKVFHLSYLHNCETRRGQILLWSGSKVFEELTDIERQFHKALYTVRAFLNCDRY 275
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A;Experimental source: strain Bristol N2; clone C32E12
                                         114 PFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYL 113
   IAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCERCSVLL 177
                                                                                                                                                                                                                                                                                                                                                                         C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYL
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A;Introns: 52/2: 137/2: 166/2: 217/3: 327/2
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase homology
F;189-393/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology
                                                                                                                                                                                                                                                                                                                                            ,5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) alpha chain - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: $13030; MUID: 91130581; PMID:1847109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Description: The sequence of C. elegans cosmid C32E12. A; Reference number: 220055

    Caenorhabditis elegans

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 183; DB 2;
Pred. No. 4.5e-07;
7; Mismatches 54
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A;Molecule type: DNA
A;Residues: 1-393 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.8%;
34.1%;
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Best Local Similarity 34.18
Matches 43; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 SVLLLE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       II II:
SVGLLD 281
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Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: CESP: C32E12.2
                                                                                                                                                              |:
LD 279
                                                                                                                           LE 179
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                                                                                                                           178
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#42281
3 / 5' -cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta chain - human
C:Species; Homo sapiens (man)
C:Decies; Homo sapiens (man)
R:Collins; C.: Hutchinson, G.: Kowbel, D.; Riess, O.; Weber, B.: Hayden, M.R.
Genomics 13, 698-704, 1992
A:Title: The human beta-subunit of rod photoreceptor cGMP phosphodiesterase: complete re
A:Reference number: S48288 (MID:92347868; PMID:1322354
A:Reference number: S48288 (MID:92347868; PMID:1322354
A:Rocious type: mRNA
A:Residues: 1-844 <CGD>
A:Coss-references: GB:541458; NID:9252525; PTDN:AAB22690.1; PID:925253
A:Rocious csequence extracted from NCBI backbone (NCBIN:109783, NCBIP:109784)
A:Rocious csequence extracted from NCBI backbone (NCBIN:109783, NCBIP:109784)
A:Rocious csequence extracted from NCBI backbone (NCBIN:109783, NCBIP:109784)
A:Rocious csequence art and photoreceptor cdp phosphodiesterase beta-subunit. Structural stu
A:Residues: 1844 <CMB-
A:Residues: 1845 <CMB-
A:Residues: 1845 <CMB-
A:Residues: 1845 <CMB-
A:Residues: 1845 <CMB-
A:Residues: Ress. 19, 6253-6268, 1991
A:Title: Genomic organization and complete sequence of the human gene encoding the beta-
A:Residues: 1.314, Q',316-319, L',321-359, R',361-697, I',699-854 <WEB>
A:Residues: 1.314, Q',316-319, L',321-359, R',361-697, I',699-854 <WEB>
A:Residues: GDR:Propences: GDR:Propences
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A;Map position: 4p16.3-4p16.3
C;Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide C;Superfamily: 3',5'-cyclic-nucleotide C;Keywords: cGMP binding: phosphoric diester hydrolase
F;556-789/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
                            A;Cross-references: EMBL:223014; NID:g312327; PIDN:CAA80557.1; PID:g312328
C;Superfanily: 3',5'-cyclic-Camp phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide
C;Keywords: cGMP binding; phosphoric diester hydrolase
F;556-789/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 FNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYLPFCG 117
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                                                                                                                                                                                    856;
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                                                                                                                                                                              19.1%; Score 186; DB 1; Length 85 34.3%; Pred. No. 2.6e-07; ive 26; Mismatches 60; Indels
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A; Residues: 1-184, 'D', 186-856 <CLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AYLNCDRYSVGLLD 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 TLLKCERCSVLLLE 179
                                                                                                                                                                                                                                             46; Conservative
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Best Local Similarity
Matches 46; Conserv
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Best Local 8
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Gaps

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Length 859; 54; Indels 3

Gaps

3;

Indels

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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; WUID:21595285; PMID:11759840
                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1.2, X', 4.6, 6-18, 'S', 20-48, 'DV', 51-157, 'T', 159-175, 'C', 177-231, 'R', 233-
A; Residues: 1.2, X', 4.6, 6-18, 'S', 20-48, 'DV', 51-157, 'T', 159-175, 'C', 177-231, 'R', 233-
A; Cross-references: EMBL: X55968; NID: 953616; PIDN: CAA39439.1; PID: 953617
A; Note: the authors translated the codon AGA for residue 232 as Glu
C; Superfamily: 3', 5' cyclic-GMP phosphodiesterase alpha chain; 3', 5' cyclic-nucleotid
C; Keywords: cGMP binding: phosphoric diester hydrolase
F; 556-789/Domain: 3', 5' cyclic-nucleotide phosphodiesterase homology <CNP>
                                                                                                                   A;Title: Retinal degeneration in the rd mouse is caused by a defect in the beta subun A;Reference number: S13121; MUID:91015387; PMID:1977087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C;Accession: AB2044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46 LIQRQTKTKDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDD 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EKVMQMYLPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQ 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 FAQKQEKITGYRTYTMLALPLLSEQGRLVAVVQLLNKLKPYSPPDALLAERIDNQGFTSA 223
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A;Cross-references: EMBL:X60133
R;Bowes, C.; Li, T.; Danciger, M.; Baxter, L.C.; Applebury, M.L.; Farber, D.B.
Nature 347, 677-680, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               adenylate cyclase [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Score 180; DB 2;
Pred. No. 7.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.1e-06
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Pred. No. 1.1e-
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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25.2%;
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34.3%;
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KELMNADRSTLWLID 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AYLNCERYSVGLLD 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46; Conservative
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Best Local Similarity
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Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-860 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
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                                                                                                                                                                             A; Accession: S13121
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                                                                                                                                                                                                             RESULT 12
$13032
3 ',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta' chain - mouse
C; Species: Mus musculus (house mouse)
C; Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jun-2000
C; Accession: $13032, $30763
R; Baehr, W.: Champagne, M.S.; Lee, A.K.; Pittler, S.J.
FEBS Lett. 278, 107-114, 1991
A; Title: Complete colMs sequences of mouse rod photoreceptor cGMP phosphodiesterase alpha A; Reference number: $13030; MUID:91130581; PMID:1847109
A; Recession: $13030; MUID:91130581; PMID:1847109
A; Residues: 1.800 cBAE>
A; Cross-references: EMBL.X60133
A; Molecule type: DNA
A; Residues: 1.800 cBAE>
A; Recession: $30762
A; Residues: 1.559, "R; 561-800 cBAE>
A; Recession: $30763
A; Molecule type: DNA
A; Residues: 1.559, "R; 561-800 cBAE>
A; Accession: $30763
A; Molecule type: DNA
A; Residues: 1.559, "R; 561-800 cBAE>
A; Cross-references: GB: X87952; EMBL:X60133; NID:g871432; PIDN:CAA61202.1; PID:g871433
A; Accession: $30763
A; Molecule type: DNA
A; Residues: 1.559, "R; 561-800 cBAE>
A; Cross-references: GB: X87952; EMBL:X60133; NID:g871432; PIDN:CAA61202.1; PID:g871433
C; Superfamily: 3', 5'-cyclic-GMP phosphodiesterase alpha chain; 3', 5'-cyclic-nucleotide phosphodiesterase homology <CNP>
C; Keywords: alternative splicing: CGMP binding; phosphoric diester hydrolase
F; 556-790/Domain: 3', 5'-cyclic-nucleotide phosphodiesterase homology <CNP>
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A;Reference number: S13030; MUID:91130581; PMID:1847109
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     330762
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta chain - mouse
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta chain - mouse
C;Species: Mus musculus (house mouse)
C;Species: Nov-1993 #sequence_revision 19-Oct-1995 #text_change 21-Jan-2000
C;Accession: S30762; S13031; S13121
R;Baehr, W.
R;Reference number: S30762
A;Reference number: S30762
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-856 <BAE>
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R;Baehr, W.; Champagne, M.S.; Lee, A.K.; Pittler,
FEBS Lett. 278, 107-114, 1991
                                                                                      114 PFCGIAISNAQLFAASRKEYERSRALLEVV 143
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Matches 46; Conserv
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A; Status: preliminary
A; Molecule type: mRNA
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C;Species: Nostoc sp.
A;Note: Nostoc sp.
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Accession: AC2089
R;KaneKo, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriquchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.; A;Itie: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-859 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB73965.1; PID:g17131357; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 PFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKC 170
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e-06;
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Search completed: June 13, 2003, 15:49:43 Job time : 8.51253 secs

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GenCore version 5.1.6
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- protein search, using sw model OM protein June 13, 2003, 15:38:49; Search time 3.97722 Seconds (without alignments) 2023.123 Million cell updates/sec Run on:

US-09-663-542-1_COPY_1_194 975 1 MLKQARRPLFRNVLSATQWK......VLLLEDIESPVVKFTKSFEL 194 Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	m	56 bos t	16 can	homo	gallus	bos tau	P51160 homo sapien	bos t		homo	canis			P91119 caenorhabdi	P23440 mus musculu	bos t	homo	рошо	rattu	P14099 bos taurus	P30645 caenorhabdi			P45970 caenorhabdi		Q00798 plasmodium		O66652 aquifex aeo		22	8955	8982	9zdu3
SUMMARIES	4	TD	CN5A_RAT	CN5A_BOVIN	CN5A_CANFA	CN5A_HUMAN	CNRC_CHICK	CNRC_BOVIN	CNRC_HUMAN	CNRA_BOVIN	CNRA_HUMAN	CNRB_HUMAN	CNRB_CANFA	CNRA_MOUSE	CNRA_CANFA	YBZJ_CAEEL	CNRB_MOUSE	CNRB_BOVIN	CN10_HUMAN	CN2A_HUMAN	CN2A_RAT	CN2A_BOVIN	YNE6_CAEEL	MY5A_HUMAN	IMDH_METJA	LINS_CAEEL	MY5A_RAT	RBP1_PLAVB	MY5A_MOUSE	MUTS_AQUAE	TRX_DROME	POLG_HRV16	- 1	YF87_METJA	Y231_RICPR
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Q45120 bacteroides	013864 schizosacch		P35748 oryctolagus	P23239 xenopus lae	Q9c469 schizosacch	Q9uzc8 pyrococcus	Q96aa8 homo sapien		067887 aquifex aeo	
ISTB_BACFR	IMB1_SCHPO	RA50_PYRFU	MYHB_RABIT	DESM_XENLA	GRT1_SCHPO	RA50_PYRAB	Y555_HUMAN	SMC1_YEAST	UVRC_AQUAE	YC06_KLEPN
Н.	-	Н	٦	Н	-	-	~	Н	, - 1	-
263	863	882	1972	458	648	880	810	1225	266	722
8.1	8.1	8.1	8.1	8.0	8.0	8.0	7.9	7.9	7.9	7.9
78.5	.78.5	78.5	78.5	7.8	7.8	7.8	77.5	77.5	77	77
34	30	37	38	39	40	4.1	42	43	44	4.5

ALIGNMENTS

RESULT 1 CN5A_RAT	CN5A_RAT STANDARD; PRT; 833 AA.	054735;	15-JUL-1999 (Rel. 38, Created)	15-JUL-1999 (Rel. 38, Last sequence update)	15-JUN-2002 (Rel. 41, Last annotation update)	Ť		_	Rattus norvegicus (Rat).		Mammalia; Eutheria; Rodentia; Sciuroquathi; Muridae; Murinae; Rattus.				STRAIN=Sprague-Dawley; TISSUE=Lung;	MEDLINE=98036118; PubMed=9370351;	Kotera J., Yanaka N., Fujishige K., Imai Y., Akatsuka H., Ishizuka T.,		"Expression of rat cGMP-binding cGMP-specific phosphodiesterase mRNA	•~		-!- FUNCTION: PLAYS A ROLE IN SIGNAL TRANSDUCTION BY REGULATING THE	INTRACELLULAR CONCENTRATION OF CYCLIC NUCLEOTIDES. THIS	
¥ 5	11	AC	딥	5	70	DE	DE	S. G.	SO	8	8	õ	RN	RP	RC	K.Y	RA	RA	RT	RT	RL	ည	ပ္ပ	ر

PHOSPHODIESTERASE CATALYZES THE SPECIFIC HYDROLYSIS OF CGMP TO 5'-ঘ

-!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)0 = guanosine 5'-phosphate.
-!- COFACTOR: REQUIRES DIVALENT CATIONS. INC IONS ARE REQUIRED FOR MAXIMUM ACTIVITY. MANGANESE, MAGNESIUM AND COBALT ALSO SUPPORT CATALYSIS BUT AT WUCH HIGHER CONCENTRATIONS (BY SIMILARITY).
-!- PATHWAY: CYCLIC INCLEOLIGE metabolism.
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS: PDE5A1 AND PDE5A2 (SHOWN HERE);
ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- DATALYSIS BUT AT MATAL SITES AND AN N-TERMINAL REGULATORY DOMAIN: COMPOSED OF A C-TERMINAL CAPALYTIC DOMAIN COMPOSED OF A C-TERMINAL CAPALYTIC DOMAIN COMPOSED OF A G-TERMINAL REGULATORY DOMAIN WHICH CONTAINS TWO HOMOLOGOUS ALLOSTERIC CGMP-BINDING REGIONS, A

AND B.

PTM: PHOSPHORYLATION IS REGULATED BY BINDING OF CGMP TO THE TWO ALLOSTERIC SITES (BY SIMILARITY).
SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE +

FAMILY '.

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InterPro; IPR003018; GAF. InterPro; IPR003607; ME_Pplase_HDc. InterPro; IPR002073; PDEase. EMBL; D89093; BAA23672.1; -. 35555555555555555555555555555555

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MUTAGENESIS
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NP_BIND
                                                                                                                                               binding
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 7
                                                                                                                                                                                                                                                                                                           113 LPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCER 172
                                                                                                                                                                                                                                                                                                                      54 KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAIN-KIPEGAPFTEDDEKVMQMY
                                              PROSITE; PS00126; PDEASE_I; 1.
Hydrolase; cGMP; cGMP-binding; Phosphorylation; Alternative splicing;
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (SA) - cyclic phosphodiesterase (EC 3.1.4.17) (CGB-PDE)
(CGMP-binding cGMP-specific phosphodiesterase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Francis S.H., Colbran J.L., McAllister-Lucas L.M., Corbin J.D.,
Lanc interactions and conserved motifs of the cGMP-binding cGMP-
specific phosphodiesterase suggest that it is a zinc hydrolase.";
J. Biol. Chem. 269:22477-22480(1994).
                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                 DB 1; Length 833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McAllister-Lucas L.M., Sonnenburg W.K., Kadlecek A., Seger D.
Trong H.L., Colbran J.L., Thomas M.K., Walsh K.A., Francis S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corbin J.D., Beavo J.A.;

"The structure of a bovine lung cGMP-binding, cGMP-specific
"The structure of a howine lung cGMP-binding, cGMP-specific
                                                                                                               CGMP (BY SIMILARITY)
CGMP (BY SIMILARITY)
CATALYTIC (BY SIMILARITY)
PHOSPHORYLATION (POTENTIAL).
ZINC 1 (POTENTIAL).
ZINC 1 (POTENTIAL).
ZINC 1 (POTENTIAL).
ZINC 2 (POTENTIAL).
                                                                                                                                                                                                                                                    Indels
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                                                                           (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                      SIMILARITY).
                                                                                                                                                                                                                                                    43;
                                                                                                                                                                                                                                Score 308.5; DB 1 Pred. No. 1.7e-18;
                                                                                                                                                                                                                         31.6%; Sco...
43.7%; Pred. No. 1...
... 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phosphodiesterase deduced from a cDNA clone.
J. Biol. Chem. 268:22863-22873(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                  865 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                            |::::: | | |:: |:: | CTIFIVD--EDCPDSFSRVFQM 344
                                                                                                                                                                                                                                                                                                                                                 CSVLLLEDIESPVVKFTKSFEL 194
                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                      CGMP
CGMP
CGMP
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MEDLINE=94043054; PubMed=8226796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-94357882; PubMed-8077192;
                  PDIESTERASE1.
                                                                                                                                                                                                              94556 MW;
Pfam; PF00233; PDEase; 1.
                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                     468
244
245
257
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615
640
                            SMART; SM00065; GAF; 2. SMART; SM00471; HDC; 1.
                                                                                                                         446
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571
575
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           GAF; 2
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                                                                                                                                                                                                                       Query Match
Best Local Similarity
Thes 62; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
                                                                                                                                                                                                             833 AA;
                 PRINTS; PR00387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDE5A OR PDE5
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                                                                   Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                CN5A_BOVIN
Q28156;
                                                                                                                                                                                                                                                                                                                              265
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BINDING
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DOMAIN
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                                                                   Zinc;
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphorylation.";
Biochem, J. 329:505-510(1998).
-!- FUNCTION: PLAYS A ROLE IN SIGNAL TRANSDUCTION BY REGULATING THE
-!- FUNCTION: PLAYS A ROLE IN SIGNAL TRANSDUCTION BY REGULATING THE
NITRACELLULAR CONCENTRATION OF CYCLIC NUCLEOTIDES. THIS
PHOSPHODIESTERASE CATALYZES THE SPECIFIC HYDROLYSIS OF CGMP TO 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PATHWAY: Cyclic nucleotide metabolism.
DOMAIN: COMPOSED OF A C-TERMINAL CAPALYTIC DOMAIN CONTAINING TWO PUTATIVE DIVALENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN WHICH CONTAINS TWO HOMOLOGOUS ALLOSTERIC CGMP-BINDING REGIONS, A
                                                                                                                                                                                                                                                                                            MEDLINE=96355629; PubMed=8703039;
Turko I.V., Halk T.L., McAllister-Lucas L.M., Burns F., Francis S.H.
Francis S.H., Corbin J.D.;
"Identification of key amino acids in a conserved cGMP-binding site
cGMP-binding phosphodiesterases. A putative NKXND motif for cGMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION IS REGULATED BY BINDING OF CGMP TO THE TWO
                                  McAllister-Lucas L.M., Haik T.L., Colbran J.L., Sonnenburg W.K., Seger D., Turko I.V., Beavo J.A., Francis S.H., Corbin J.D.; Ah essential aspartic acid at each of two allosteric cGMP-binding sites of a cGMP-specific phosphodiesterase."; J. Biol. Chem. 270:30671-30679(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTM: PHOSPHORYLATION IS REGULATED BI BINDING OF COMMISSION SITES.

ALLOSTERIC SITES.
SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)O · guanosine 5'-phosphate.
COFACTOR: REQUIRES DIVALENT CATIONS. ZINC IONS ARE REQUIRED FYMAXIMUM ACTIVITY. MANGANESE, MAGNESIUM AND COBALT ALSO SUPPOR CATALYSIS BUT AT MUCH HIGHER CONCENTRATIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENZYME REGULATION: MOST POTENTLY INHIBITED BY ZAPRINAST AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Turko I.V., Francis S.H., Corbin J.D.; "Binding of cGMP-binding cGMP-specific phosphodiesterase (PDE5) is required for its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PSO0126; PDEASE_I; 1.
Hydrolase; cGMP; cGMP-binding; Phosphorylation; Zinc; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOSPHORYLATION (POTENTIAL)
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ZINC 1 (POTENTIAL).
ZINC 1 (POTENTIAL).
ZINC 2 (POTENTIAL).
ZINC 2 (POTENTIAL).
ZINC 2 (POTENTIAL).
CGMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol. Chem. 271:22240-22244(1996).
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InterPro, IPR003607; ME_Pplase_HDc.
InterPro, IPR002073; PDEase.
MEDLINE=96107229; PubMed=8530505;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOSPHORYLATION, AND MUTAGENESIS
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PRINTS: PR00387; PDIESTERASE1.
SMART; SM00065; GAF: 2.
SMART; SM00471; HDC: 1.
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607
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672
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CTIFIVDE 364
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                                                                                                                                                                     FAMILY.
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                                                                                                       AND B.
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                                                                                                                   PTM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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METAL
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                                                                                                                                                                                                                                                                                                        LPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCER 172
                                                                                                                                                                                                                                                                                                                    E->A: NO CHANGE IN CGMP-BINDING.
D->A: INCREASED CGMP-BINDING; NO CHANGE
IN CATALYTIC ACTIVITY. PHOSPHORYLATED AT
LOWER CONCENTRATIONS OF CGMP.
2FF7144b299084F7 CRC64;
                                                                                                                                                                                                                                                                         N->A: DECREASED CGM-BINDING; NO CHANGE
                                                                                                               D->A: DECREASED CGMP-BINDING; NO CHANGE IN CATALYTIC ACTIVITY.
                                                                                  NO CHANGE
                                                                                                                                   D->N: INCREASED CGMP-BINDING; NO CHANGE IN CATALYTIC ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                               077746; 077747;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
CGMP-specific 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (CGB-PDE)
PDE5A OR PDE5.

    Biol. Chem. 273:26982-26990(1998).
    FUNCTION: PLAYS A ROLE IN SIGNAL TRANSDUCTION BY REGULATING THE
INTRACELLULAR CONCENTRATION OF CYCLIC NUCLEOTIDES. THIS
PHOSPHODIESTERASE CATALYZES THE SPECIFIC HYDROLYSIS OF CGMP TO

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)0 = guanosine 5'-phosphate.
COFACTOR: REQUIRES DIVALENT CATIONS. ZINC IONS ARE REQUIRED FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kotera J., Fujishige K., Akatsuka H., Imai Y., Yanaka N., Omori K.;
"Novel alternative splice variants of cGMP-binding cGMP-specific
phosphodiesterase.";
                                                                                K->A: DECREASED CGMP-BINDING; NO CHANG
IN CATALYTIC ACTIVITY.
K->R: SLIGHT INCREASE IN CGMP-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAXIMUM ACTIVITY. MANGANESE; MAGNESIUM AND COBALT ALSO SUPPORT CATALYSIS BUT AT MUCH HIGHER CONCENTRATIONS (BY SIMILARITY). ENZYME REGULATION: INHIBITED BY ZAPRINAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PATHWAY: Cyclic nucleotide metabolism.
SUBCELLULAR LOCATION: PDE5A1 AND PDE5A2 ARE LOCATED MOSTLY TO
SOLUBLE CELLULAR FRACTIONS AND SOME TO PARTICULATE CELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis
                                                                                                                                                                                                                      DB 1; Length 865;
                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                    31.5%; Score 307.5; DB 1;
46.1%; Pred. No. 2.2e-18;
live 31; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS PDE5A1 AND PDE5A2).
                                        CGMP.
CATALYTIC (
                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98434620; PubMed=9756948;
                                                                                                                                                                                                  MW.
                                                                                                                                                                                                865 AA; 98626
                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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357 CTIFIVDE 364
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nes 59; Conserv
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                                                                                                                                   289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAIN-KIPEGAPFTEDDEKVMQMY 112
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CATALYTIC (BY SIMILARITY).
PHOSPHORYLATION (POTENTIAL).
ZINC 1 (POTENTIAL).
ZINC 1 (POTENTIAL).
ZINC 2 (POTENTIAL).
MERGSPGAGARLPRODDSVEAMLDDHRDFTFSYFVKKAT
                       ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: BOTH ISOFORMS EXPRESSED ABUNDANTLY IN THE
CEREBELLUM, HIPPOCAMPUS, RETINA, LUNG, HEART, SPLEEN, AND THORACIC
ARTERY PDE5A1, BUT NOT PDE5A2, IS ALSO ABUNDANTLY EXPRESSED IN
                                                                                                                                                                                                                                                                                                     ALLOSTERIC SITES (BY SIMILARITY).

NESCELLANEOUS: CGMP-BINDING TO THE ALLOSTERIC SITES IS STIMULATED BY 3-ISOBUTYL-1-METHYLXANITHUR (IBMX).
SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00126; PDEASE_1; 1.
Hydrolase; cGMP; cGMP-binding; Phosphorylation; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
  PDE5A1 (SHOWN HERE) AND PDE5A2;
                                                                                                                                                            DOMAIN: COMPOSED OF A C-TERMINAL CATALYTIC DOMAIN CONTAINING TWO PUTATIVE DIVALENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN WHICH CONTAINS TWO HOMOLOGOUS ALLOSTERIC CGMP-BINDING REGIONS, A
                                                                                                                                                                                                                                                                           PHOSPHORYLATION IS REGULATED BY BINDING OF CGMP TO THE TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -> MLPFGHQR (IN ISOFORM PDE5A2)
F20BB37B71E93BB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGMP (BY SIMILARITY). CGMP (BY SIMILARITY).
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(BY SIMILARITY)
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  2 ISOFORMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro, IPR003018; GAF.
InterPro, IPR003607; ME_Pplase_HDc.
InterPro, IPR002073; PDEase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGMP
CGMP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00387; PDIESTERASE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.18;
ALTERNATIVE PRODUCTS:
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SMART; SM00471; HDC;
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genew;
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CGMP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECUENCE FROM N.A. (ISOFORM PDESA1).

TISSUE=Prostate, and Skeletal muscle;

MEDLINE=98308101; PubMed=9642111;

Stacey P., Rulten S., Dapling A., Phillips S.C.;

"Molecular cloning and expression of human cGMP-binding cGMP-specific phosphodiesterase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LESSER EXTENT, IN BRAIN, LIVER AND LUNG.
DOMAIN: CORPOSED OF A C-TERMINAL CATALYTIC DOMAIN CONTAINING TWO PUTATIVE DIVALENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN WHICH CONTAINS TWO HOWOLOGOUS ALLOSTERIC COMP-BINDING REGIONS, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)0 = guanosine 5'-phosphate.

GORACDA: REQUIRES DIVALENT CATIONS: ZINC IONS ARE REQUIRED FOR MAXIMUM ACTIVITY. MANGANESE, MAGNESIUM AND COBALT ALSO SUPPORT CATALYSIS BUT AT MOCH HIGHER CONCEMPRATONS (BY SIMILARITY).

ENZYME REGULATION: SILDENAFIL (VIAGRA) IS A HIGHLY SELECTIVE AND POTBNT INHIBATOR OF PDESA AND IS EFFECTIVE IN THE TREATMENT OF PENILE ERECTILE DYSFUNCTION. ALSO INHIBITED BY ZAPRINAST.

PATHWAY: CYCLIC nUCLEOCLIGE metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PLAYS A ROLE IN SIGNAL TRANSDUCTION BY REGULATING THE INTRACELLULAR CONCENTRATION OF CYCLIC NUCLEOTIDES. THIS PHOSPHODIESTERASE CATALYZES THE SPECIFIC HYDROLYSIS OF GGMP TO 5'
                                 CNSA_HUWAN STANDARD, PRT; 875 AA.
076074; 075887; 075026; 097626;
15-JUL-1999 (Rel. 38, created)
15-JUL-1999 (Rel. 38, rast sequence update)
15-JUL-1999 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
cGMP-specific 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (CGB-PDE)
PDE5A OR PDE5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTM: PHOSPHORYLATION IS REGULATED BY BINDING OF CGMP TO THE TWO ALLOSTERIC SITES (BY SIMILARITY).
SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
                                                                                                                                                                                                                                                                                                                                                   TISSUE-Placenta, and Lung;

MEDLINE-98380237; Pubmed-9716380,

Yanaka N., Kotera J., Ohtsuka A., Akatsuka H., Imai Y., Michibata I.

Fujishige K., Kawai E., Takebayashi S.-I., Okumura K., Omori K.;

Expression, structure and chromosomal localization of the human cGMP-binding GMP-specific phosphodlesterase PDE5A gene.";

Eur. J. Blochem. 255:391-399(1998).
                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                            MEDLINE-98382582; PubMed-9714779; Loughney K., Hill T.R., Florio V. A., Uher L., Rosman G.J., Wolda Jones B.A., Howard M.L., McAllister-Lucas L.M., Sonnenburg W.K., Francis S.H., Corbin J.D., Beavo J.A., Ferguson K.; Tsolation and characterization of cDNAs encoding PDE5A, a human binding, CGMP-specific 3',5'-cyclic nucleotide phosphodiesterase Gene 216:139-147(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: EXPRESSED IN AORTIC SMOOTH MUSCLE CELLS,
HEART, PLACENTA, SKELETAL MUSCLE AND PANCREAS AND, TO A MUCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kotera J., Imai Y., Omori K.; "Molecular cloning and characterization of human cGMP-specific phosphodiesterase 5A2 cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem. Biophys. Res. Commun. 247:249-254(1998).
                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS PDE5A1 AND PDE5A2).
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM PDE5A1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM PDE5A2)
                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphodiesterase.
                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND
                         CN5A_HUMAN
           RESULT
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                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PHOSPHORYLATION (POTENTIAL).
ZINC 1 (POTENTIAL).
ZINC 1 (POTENTIAL).
ZINC 2 (POTENTIAL).
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Hydrolase; cGMP; cGMP-binding; Phosphorylation; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESYFVRKA -> MLPFGDK (IN ISOFORM PDE5A2)
MISSING (IN REF. 2; BAA33372).
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91EA8C33B6CD254D CRC64;
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Pred. No. 2.2e-18;
1; Mismatches 37;
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InterPro; IPR003607; ME_Pplase_HDc.
InterPro; IPR002073; PDEase.
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                                                                                                                                                                                                                                                                      EMBL; AF043731; AAC63967.1; -. :
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Pfam; PF01590; GAF; 2.
PRINTS; PR00387; PDIESTERASE1.
                                                                                                                                                                                                                                                                                                  AF04865; CAA06170.1; -A0004865; CAA06170.1; -AB001615; BAA33372.1; -AB001616; BAA33372.1; JAB001616; BAA33372.1; JAB001617; JAB001617; BAA33372.1; JAB001617; JAB00161
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46.1%;
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AB001628; BAA33372.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AB001623;
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Best Local S
Matches 59
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112 TRLLNVTPTS-----KFEDNLVNPDKETVFPLDIGIAGWVAHTKKFFNIPDVKKNNHFS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from a cDNA clone.";
Proc. Natl. Acad. Sci. U.S.A. 87:293-297(1990).
                                                                                                                                                                                                                                                                                    AA
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PIR; A34810; A34810.
Interpro; IPR003018; GAF.
Interpro; IPR002073; PDEase.
Interpro; IPR0012073; PDEase.
Fram: PP00133; PDEase; IPR001203; PDEase; IPR001203; PDEase; IPR001203; PDEase; IPR001500; GAF; 2.
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SMART; SM00065; GAF; 2.
SMART; SM00471; HDC; 1.
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                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                        PDE6C OR PDEA2
                                                                                                                                                                                                                                                                                CNRC_BOVIN
P16586;
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                                                                                                                                 -KDRRFN 59
                        KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAIN-KIPEGAPFTEDDEKVMQMY
                                             Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phaslanidae; Phaslaninae;
                                                                                                          LPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDILINE-55121406; PubMed=7821382;
Semple-Rowland S.L., Green D.A.;
"Molecular characterization of the alpha'-subunit of cone
photoreceptor cGMP phosphodiesterase in normal and rd chicken.";
Exp. Eye Res. 59:356:372(1994).
-:- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)0 =
quanosine 5'-phosphate.
-:- SUBUNIT: COMPOSED OF TWO ALPHA' SUBUNITS THAT ARE ASSOCIATED
WITH 3 SMALLER PROTEINS OF 11, 13, AND 15 kDa.
-:- SIMILARIY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Cone cGMP-specific 3',5'-cyclic phosphodiesterase alpha'-subunit (EC 3.1.4.17).
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Hydrolase; CGMP; Vision; Prenylation; Lipoprotein; Membrane.
LIPID 859 859 GERANYL-GERANYL (BY SIMILARITY).
SEQUENCE 862 AA; 100008 MW; BD3145BB5FF826A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.1%; Score 205.5; DB 1; 29.4%; Pred. No. 8.5e-10; Live 34; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                 862 AA.
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STRAIN-Rhode Island red; TISSUE-Retina;
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InterPro; IPR003607; ME_Pplase_HDC.
InterPro; IPR002073; PDEase.
InterPro; IPR001230; Prenyl_site.
Pfam; PF01590; GAF; 2.
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SMART; SM00065; GAF; 2.
SMART; SM00471; HDC; 1.
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CTIFIVDE 374
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Best Local Similarity
Matches 53; Conserv
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                                                                                                                                                                                                                                                                                                                                               CNRC_CHICK
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
DEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYLPFCGIA 119
                                                                                                                                                                                                   120 ISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCERCSVLLLE 179
                                                                                                                                                                                                                                                   LRNHHTSYLYNIESRRSQMLLWSANKVFEELTDIERQFHKALYTIRMYLNCERYSVGLLD 283
                                                          | :|| || | | ::: :|| : || :|| || || :|| DYLDKKTGYTTVNMMAIPI-TQGKEVLAVVMALNKL-NASEFSKEDEEVFKKYLNFISLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
MEDLINE=90115860; PubMed=2153291;
MEDLINE=9011586.
Li T., Volpp K., Applebury M.L.;
"Bovine cone photoreceptor cGMP phosphodiesterase structure deduced "Bovine cone photoreceptor cGMP phosphodiesterase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 87:288-292(1990).
-!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)0 = guanosine 5'-phosphate.
-!- SUBUNIT: COMPOSED OF TWO ALPHA' SUBUNITS THAT ARE ASSOCIATED WITH 3 SMALLER PROTEINS OF 11, 13, AND 15 kDa.
-!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
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Sukaryota: Metazooa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1990 (Rel. 15, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Cone cGMP-specific 3',5'-cyclic phosphodiesterase alpha'-subunit
(EC 3.1.4.17) (PDE V-C1).
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Hydrolase; cGMP; Vision; Prenylation; Lipoprotein; Membrane.
LIPID 852 852 GERANYL-GERANYL (BY SIMILARITY).
SEQUENCE 855 AA; 98797 WW; IFCFFPD045686D65 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Identification of a noncatalytic cGMP-binding domain conserve both the cGMP-stimulated and photoreceptor cyclic nucleotide phosphodiesterases.";
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SEQUENCE OF 308-502 FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-90115859; PubMed=2153290;
Charbonneau H., Prusti R.K., Letrong H., Sonnenburg W.K.,
Mullaney P.J., Walsh K., Beavo J.A.;
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278
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                                                                                                                                                        212
                                                                                                                                                                                              54 KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYL 113
                                                                                                                                       "Gene structure and amino acid sequence of the human cone photoreceptor cGMP-phosphodiesterase alpha' subunit (PDEA2) and its chromosomal localization to 10q24."; Genomics 28:429-435(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: COMPOSED OF TWO ALPHA' SUBUNITS THAT ARE ASSOCIATED WITH 3 SMALLER PROTEINS OF 11, 13, AND 15 kDa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-07T-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Cone cGMP-specific 3',5'-cyclic phosphodiesterase alpha'-subunit
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                   Length 855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Piriev N.I., Viczian A., Ye J., Farber D.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Feshchenko E.A.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
-!- CATALYWIC ACTIVITY: Guanosine 3',5'-cyclic phosphate
guanosine 5'-phosphate.
           Query Match 20.0%; Score 195; DB 1; Best Local Similarity 36.5%; Pred. No. 6.5e-09; Matches 46; Conservative 25; Mismatches 53
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MEDLINE=96039253; PubMed=7490077;
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AAA92886.1;
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                                                                                                                                                                                                                                                                                           SVLLLE 179
                                                                                                                                                                                                                                                                                                                        |: ||:
273 SIGLLD 278
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SEQUENCE FROM N.A.
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PDE6C OR PDEA2.
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U20197; P
U20199; P
U20200; P
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AAA92886.1;

EMBL; EMBL;

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114 PFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218 NFVSIILRLHHTSYMYNIESRRSQILMWSANKVFEELTDVERQFHKALYTVRSYLNCERY 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-90169986; PubMed-2155175; Pittler S.J., Bachr W., Wasmuth J.J., McConnell D.G., Champagne M.S., Vantuinen P., Ladbetter D., Davis R.L.; McDecular characterization of human and bovine rod photoreceptor cGMP phosphodiasterase alpharsubunit and chromosomal localization of Genomics 6:272-283(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                  GERANYL-GERANYL (BY SIMILARITY).
V -> D (IN REF. 3).
Q -> P (IN REF. 3).
Q -> P (IN REF. 1).
P -> L (IN REF. 1).
Q -> R (IN REF. 1).
W, 3D1535C21780A56E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1989 (Rel. 12, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Rod cGMP-specific 3',5'-cyclic phosphodiesterase alpha-subunit (EC 3.1.4.17) (GMP-PDE alpha) (PDE V-Bl).
                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00126; PDEASE_I; 1.
Hydrolase; cGMP; Vision; Prenylation; Lipoprotein; Membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.6%; Score 191; DB 1; 36.5%; Pred. No. 1.4e-08; iive 24; Mismatches 54;
                                                                                                                                                                                                                                          InterPro; IPR003607; ME_Pplase_HDc.
InterPro; IPR002073; PDEase.
InterPro; IPR001230; Prenyl_site.
                                                                                                                              JOINED.
                                     JOINED
                                                    JOINED
                                                                          JOINED
                                                                                           JOINED
                                                                                                               JOINED
                                                                                                                                                                                                                                                                                                                                      PRINTS, PR00387; PDIESTERASE1.
SMART, SM00065; GAF, 2.
SMART, SM00471; HDc, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99102 MW:
                                 . U20205; AAA92886.1; J
. U20206; AAA92886.1; J
. U20207; AAA92886.1; J
. U20208; AAA92886.1; J
. U20209; AAA92886.1; J
                                                                                                                             U20210; AAA92886.1;
U20211; AAA92886.1;
X94354; CAA64079.1;
AAA92886.1;
AAA92886.1;
                                                                                                                                                                                                                                                                                                 Pfam; PF00233; PDEase; 1.
Pfam; PF01590; GAF; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                      InterPro; IPR003018; GAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                   HGNC:8787; PDE6C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               174 SVLLLE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   858 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGLLD
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P11541;
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                                                                                                                           Lipkin V.M.; "Cyclic GMP phosphodiesterase from the bovine retina. Amino acid sequence of the alpha-subunit and nucleotide sequence of corresponding
                                                                                                                                                                                                                                                                          Ovchinnikov Y.A., Gubanov V.V., Khramtsov N.V., Ischenko K.A., Zagranichny V.E., Muradov K.G., Shuvaeva T.M., Lipkin V.M.; "Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence of the alpha-subunit and nucleotide sequence of the corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                          guanosine 5'-phosphate.
SUBUNIT: OLIGOMER COMPOSED OF TWO CATALYTIC CHAINS (ALPHA AND BETA), AN INHIBITONY CHAIN (GAMMA) AND THE DELTA CHAIN.
SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
                                                                                                                                                                                                                                                                                                                                                         FEBS Lett. 223:169-173(1987).
-!- FUNCTION: THIS PROTEIN PARTICIPATES IN PROCESSES OF TRANSMISSION AND AMPLIFICATION OF THE VISUAL SIGNAL.
-!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)0
                                                             Yu A., Ovchinnikov A., Gubanov V.V., Khramtsov N.V., Akhmedov N.B., Ishchenko K.A., Zagranichnyi V.E., Vasilevskaya I.A., Rakitina T.V., Atabekova N.V., Barinov A.A., Muradov K.G., Shuvaeva T.M., Bystrov N.S., Severtsova I.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS00126; PDEASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M -> V.
V -> A (IN REF. 2 AND 3).
T -> A (IN REF. 2 AND 3).
F -> C (IN REF. 2 AND 3).
N; 86624E43662A95CC CRC64).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACETYLATION.
FARNESYL (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.4%; Score 189; DB 1; 33.3%; Pred. No. 2.1e-08;
                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                             Dokl. Akad. Nauk SSSR 296:487-491(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; S06418; S06418.
PIR; A34611; A34611.
InterPro; IPR003018; GAF.
InterPro; IPR003607; ME_Pplase_HDc.
InterPro; IPR002073; PDBase.
InterPro; IPR001230; Prenyl_site.
                                            MEDLINE-88082056; PubMed-2826095;
                                                                                                                                                                                                                                                            MEDLINE=88030033; PubMed=2822478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam: PF00233; PDESSe; 1.1.2.2.
Pfam: PF01590; GAF; 2.
PRINTS; PR00387; PDIESTERASE1.
SMART; SM00065; GAF; 2.
SMART; SM00411; HDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99209 MW;
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380
193
423
674
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                                 TISSUE-Retina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INIT_MET
MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                              CDNA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
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  PFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC 173
                       215 NFANLIMKVFHLSYLHNCETRRGQILLWSGSKVPEELTDIERQFHKALYTVRAFLNCDRY 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alpha subunit of rod cGMP phosphodiesterase.";
Nat. Genet. 11:468-471(1995)
-:- FUNCTION: THIS PROTEIN PARTICIPATES IN PROCESSES OF TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pittler S.J., Baehr W., Dryja T.P., Wasmuth J.J., McConnell D.G., Champagne M.S., Grondin V., Vantuinen P., Ledbetter D., Davis R.L.; "Molecular characterization of human and bovine rod photoreceptor complexity phosphodiesterase alpha-subunit and chromosomal localization of the human gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Autosomal recessive retinitis pigmentosa caused by mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND AMPLIFICATION OF THE VISUAL SIGNAL.

-!- CATALYTIC ACTIVITY: Guanosine 3",5'-cyclic phosphate + H(2)0 = guanosine 5'-phosphate.

-!- SUBUNIT: OLIGOMER COMPOSED OF TWO CATALYTIC CHAINS (ALPHA AND BETA), AN INHIBITORY CHAIN (GAMMA) AND THE DELTA CHAIN.

-!- DISEASE: DEFECTS IN PDE6A ARE A CAUSE OF AUTOSOMAL DOMINANT RETINITS PIGMENTOSA (ADRP) OR AUTOSOMAL RECESSIVE RP (ARRP).

PATIENTS TYPICALLY HAVE NIGHT VISION BLINDNESS AND LOSS OF MIDPERIPHERAL VISIONAL FIELD AND EVENTUALLY CENTRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WWW="http://www.retina-international.com/sci-news/pdemut.htm"
                                                                                                                                                                                                                                                               01-500. (Rel. 15, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-CTT-2001 (Rel. 40, Last annotation update)
Rod cGMP-specific 3',5'-cyclic phosphodiesterase alpha-subunit (EC 3.1.4.17) (GMP-PDE alpha) (PDE V-B1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-966083603; PubMed-7493036;
Huang S.H., Pittler S.J., Huang X:, Oliveira L., Berson E.L.,
Dryja T.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVISION TO 845-848.
Pittler S.J., Baehr W., Wasmuth J.J., McConnell D.G., Champagne M.S., Vantuinen P., Ledbetter D., Davis R.L.; Submitted (MAY-1995) to the EMBL/GenBank/DBBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DATABASE: NAME=Mutations of the PDE6A/B/G genes; NOTE=Retina International's Scientific Newsletter;
                                                                                                                                                                                                                             859 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90169986; Pubmed=2155175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M26061; AAB69155.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomics 6:272-283(1990).
                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT ARRP ARG-343.
                                                                               SVLLLE 179
                                                                                                                      SVGLLD 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VISION AS WELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                             HUMAN
114
                                                                               174
                                                                                                                      275
                                                                                                                                                                                                                               CNRA_HU
P16499;
                                                                                                                                                                                                         CNRA_HUMAN
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                                                                                                                                                                                    RESULT
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Gaps

5;

53; Indels

Pred. No. 2.1e-08;

Mismatches

29;

Conservative

42;

Matches

ò g

157

Local Similarity

54 KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYL

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VARIANT ARRP GLN-552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ERRATUM
       54 KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215 NFANLIMKWYHLSYLHNCETRRGQILLWSGSKVFEELTDIERQFHKALYTVRAFLNCDRY 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 PFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Khramtsov N.V., Feshchenko E.A., Suslova V.A., Shmukler B.E., Terpugov B.E., Rakitina T.V., Atabekova N.V., Lipkin V.M.; "The human rod photoreceptor cGMP phosphodiesterase beta-subunit. Structural studies of its CDNA and gene."; FEBS Lett. 327:275-278(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Khramtsov N.V., Feshchenko E.A., Suslova V.A., Terpugov B.E., Rakitina T.V., Atabekova N.V., Shmukler B.E., Lipkin V.M.; Structural studies of CDNA and the gene for the beta-subunit of phosphodiesterase from human relina."; Bioorg. Khim. 18:1551-1554(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CNRB_HUMAN STANDARD; PRT; 854 AA.
P35913; Q9BWH5;
01-JUN-1994 (Rel. 29, Created)
01-JUN-2002 (Rel. 29, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Rod GMP-specific 3',5'-cyclic phosphodiesterase beta-subunit (EC 31.4.17) (GMP-PDE beta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     S -> R (IN ARRP).
/FTId=VAR_006049.
983C361334D58414 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                              FARNESYL (BY SIMILARITY)
                                                                                       interPro; IRR003607; ME_Plase_HDc.
InterPro; IRR003607; ME_Plase_HDc.
InterPro; IRR001203; PDEase.
InterPro; IRR001203; PDEase.
InterPro; IRR001203; PDEase; 1.
Pfam; PF01509; GAF; 2.
Print; PR000367; PDIESTERASE1.
SMART; SM0065; GAF; 2.
PR051TE; PS00126; PDEASE_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.4%; Score 189; DB 1; 34.1%; Pred. No: 2.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.1%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Retina;
MEDLINE=93351644; PubMed=8394243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93244036; PubMed=1338685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        859 AA; 99503 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                     InterPro; IPR003018; GAF
PIR; B34611; B34611.
Genew; HGNC:8785; PDE6A.
MIM; 180071; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                       343
                                                                                                                                                                                                                                                                                                                                                                                              856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVGLLD 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 43;
                                                                                                                                                                                                                                                                                                                                                                       INIT_MET
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  DARAGE STANDAR STANDAR
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Weber B., Riess O., Hutchinson G., Collins C., Lin B., Kowbel D., Andrew S., Schappert K., Hayden M.R.;
"Genomic organization and complete sequence of the human gene encoding the beta-subunit of the cGMP phosphodiesterase and its localisation to
                                     Collins C., Hutchinson G., Kowbel D., Riess O., Weber B., Hayden M.R., "The human beta-subunit of rod photoreceptor cGMP phosphodiesterase: complete retinal cDNA sequence and evidence for expression in brain."; Genomics 13:698-704(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Retinal rod cell;
MEDITABS 5031050; PubMed=8768262;
Suslova V.A., Suslov O.N., Kim E.E., Lipkin V.M.;
Granization of the gene for the beta-subunit of human photoreceptor cyclic GMP phosphodiesterase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   blindness.";
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Gal A., Orth U., Baehr W., Schwinger E., Rosenberg T.;
Heterozygous missense mutation in the rod cGMP phosphodiesterase
"Heterozygous missense mutation in the rod cGMP phosphodiesterase
beta-subunit gene in autosomal dominant stationary night blindness
Nat. Genet. 7:64-68(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McLaughlin M.E., Sandberg M.A., Berson E.L., Dryja T.P.;
"Recessive mutations in the gene encoding the beta-subunit of rod
phosphodiesterase in patients with retinitis pigmentosa.";
Nat. Genet. 4:130-134(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A novel mutation in exon 17 of the beta-subunit of rod phosphodissterase in two RP sisters of a consanguineous family."; Hum. Genet. 97:35-38(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gao Y.Q., Danciger M., Zhao D.Y., Blaney J., Piriev N.I., Shih J. J. Acobson S.G., Heckenlively J.H., Farber D.B.; "Screening of the PDREB gene in patients with autosomal dominant retinitis pigmentosa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96140746; PubMed=8557257;
Valverde D., Solans T., Grinberg D., Balcells S., Vilageliu L.,
Bayes M., Chivelet P., Besmond C., Goossens M., Gonzalez-Duarte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-96129294; PubMed-8595886; Danciger M., Blaney J., Gao Y.Q., Zhao D.Y., Heckenlively J.R., Jacobson S.G., Farber D.B.; "Mutations in the PDE6B gene in autosomal recessive retinitis pigmentosa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gal A., Orth U., Baehr W., Schwinger E., Rosenberg
Nat. Genet. 7:551-551(1994).
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MEDLINE=96273603; PubMed=8698075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res. 19:6263-6268(1991).
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=92066478; PubMed=1720239;
MEDLINE=92347868; PubMed=1322354;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Khim. 22:256-263(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomics 30:1-7(1995).
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                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION MEMBRAND AND THE DELTA CHAIN AND SUBCELLULAR LOCATION: Membrane-associated
DISEASE: DEFECTS IN PDE6B ARE A CAUGE OF RETINITIS PICMENTOSA
DISEASE: DEFECTS IN PLOSE OF RETINITIS PICMENTOSA
OF RETINAL PHOTORECEPTOR CELLS. PATIENTS TYPICALLY HAVE NIGHT
VISION BLINDNESS AND LOSS OF MIDPERTHPRAR LEADS TO DEGENERATION
OF RETINAL PHOTORECEPTOR CELLS. PATIENTS TYPICALLY HAVE NIGHT
VISION BLINDNESS AND LOSS OF MIDPERTHPRAR LYSOLA FIELD, AS THEIR
CONDITION PROGRESSES, THEY LOOSE THEIR FAR PERIPHERAL VISIONAL
RECESSIVE (20-25 OF CASES, ARRP) AUTOSOMAL
RECESSIVE (20-25 OF CASES, ARRP) AUTOSOMAL
DISEASE; ADRP) OR X-LINKED (10-158 OF CASES, XRP) INHERITANCE.

DISEASE: DISEASE: DEFECTS IN PDE6B ARE A CAUGE OF CONGENITAL STATIONARY
             Valverde D., Baiget M., Seminago R., del Rio E., Garcia-Sandoval B., del Rio f., Bayes M., Balcells S., Martinez A., Grinberg D., Ayuso C.; "Identification of a novel R5520 mutation in exon 13 of the beta-subunit of rod phosphodiesterase gene in a Spanish family with
                                                                                                                          SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
                                                                                                                                                                                                                                                                                                                               SUBUNIT: OLIGOMER COMPOSED OF TWO CATALYTIC CHAINS (ALPHA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE-Retina International's Scientific Newsletter;
WWW-"http://www.retina-international.com/sci-news/pdemut.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DATABASE: NAME-Mutations of the PDE6A/B/G genes
                                                                               autosomal recessive retinitis pigmentosa.";
Hum. Mutat. 8:393-394(1996).
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InterPro; IPR003607; ME_Pplase_HDc.
InterPro; IPR002073; PDEase.
InterPro; IPR001230; Prenyl_site.
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EMBL; X62695; CAA62215.1; -
EMBL; X90587; CAA62215.1; -
EMBL; X90588; CAA62215.1; JOINED.
MEDLINE=97114306; PubMed=8956055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAA44569.1; JOINED.
CAA44569.1; JOINED.
CAA44569.1; JOINED.
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SMART; SM00065; GAF; 2.
SMART; SM00471; HDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; S41458; AAB22690.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIGHT BLINDNESS (CSNB3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; BC000249; AAH00249.1;
PIR; A42828, A42828.
PIR; S34590; S34590.
Genew; HGNC:8786; PDE6B.
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Pfam; PF01590; GAF; 2.
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X62694;
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FNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYLPFCG 117
                                                                                                                                                                                                                                                                                                                                                                                                                      118 IAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCERCSVLL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 LYLKIYHLSYLHNCETRRGOVLLWSANKVFEELTDIEROFHKAFYTVRAYLNCERYSVGL 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nonsense
               GGMP; Vision: Prenylation, Lipoprotein; Membrane;
pigmentosa: Disease mutation.

1 851 ROD GGMP-SPECIFIC 3',5'-CYCLIC
ROD FORM-SPECIFIC 3',5'-CYCLIC
ROSPHODIESTERASE BETA-SUBUNIT.
852 RS4 REMOVED IN MATURE FORM (BY SIMILARITY).
74 74 R-> C (IN ARRP).
75 AFIGH-VAR_009283.
166 166 E-> K (IN ARRP).
77 FIGH-VAR_009284.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN PARTICIPATES IN PROCESSES OF
TRANSMISSION AND AMPLIFICATION OF THE VISUAL SIGNAL. NECESSARY
FOR THE FORMATION OF A FUNCTIONAL PHOSPHODIESTERASE HOLDENZYME.
-!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)O =
guanosine 5'-phosphate.
-!- SUBUNIT: OLIGOMER COMPOSED OF TWO CATALYTIC CHAINS (ALPHA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBL_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                     5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN*Red setter; TISSUE=Retina;
MEDLINE=93248211; PubMed=8387203;
Suber M.L., Pittler S.J., Qin N., Wright G.C., Holcombe V.,
Lee R.H., Craft C.M., Lolley R.N., Baehr W.B., Hurwitz R.L.;
"Irish setter dogs affected with rod/cone dysplasia contain a rantation in the rod CGMP phosphodiasterase beta-subunit gene.",
Proc. Natl. Acad. Sci. U.S.A. 90:3968-3972(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last sequence update)
Rod cGMP-specific 3 , 5'-cyclic phosphodiesterase beta-subunit (EC 31.4.17) (GMP-PDE beta).
PDEGE OR PDES OR PDES.
Canis familiaris (DOG).
                                                                                                                                                                                                                                                                                                                                     Length 854;
                                                                                                                                                                                                                                 L -> H (IN ADRP AND ARRP).
/FTId=VAR_009287.
                                                                                                                                                                                                                                                                                                                                     ; Score 183; DB 1;
; Pred. No. 6.6e-08;
20; Mismatches 55;
                                                                                                                                                                                                                                                                          /FTId=VAR_009288.
H -> N (IN CSNB3)
/FTId=VAR_009289.
                                                                                                                                                                                                    Y -> H (IN ARRP)./FTId=VAR_009286
                                                                                                                                                                   Y -> H (IN ADRP)
/FTId=VAR_009285
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Clements P.J.;
PROSITE; PS00126; PDEASE_I; 1
                                                                                                                                                                                                                                                                                                                                        18.8%;
                                                                                                                                                                                                                                                                                                                                                     36.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                 219
                                                                                                                                                                      212
                                                                                                                                                                                                                               228
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                                                                                                                                                                                                                                                             228
                                  Retinitis pigmentosa;
                                                                                                                                                                                                                                                                                                                                      Query Match .
Best Local Similarity
Matches 45; Conserv
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LD 279
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                   Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                   28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178
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                                                                                            LIPID
VARIANT
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                                                 CHAIN
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    QQ
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CNRA_CANFA
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CNRA_CANFA
   QQ
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                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKVMQMYLPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQ 165
BETA), AN INHIBITORY CHAIN (GAMMA) AND THE DELTA CHAIN.
SUBCELLULAR LOCATION: Membrane-associated.
DISEASE: RIKISH SETTER DOGS AFFECTED WITH FOD/CONE DYSPLASIA (RCD1)
CONTAIN A NONSENSE WITHATON IN THE GENE THAT GIVES RISE TO A
PROTEIN OF 807 AA LACKING 49 AA IN THE C'TERMINAL.
SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHODIESTERASE BETA-SUBUNIT.
REMOVED IN MATURE FORM (BY SIMILARITY).
GERANYL-GERANYL (BY SIMILARITY).
AC9D03F6401BA132 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Rod CGMP-specific 3',5'-cyclic phosphodiesterase alpha-subunit (EC 3.1.4.17) (GMP-PDE alpha).
                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00126; PDEASE_I; 1.
Hydrolase; cGMP; Vision; Prenylation; Lipoprotein; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                    ROD CGMP-SPECIFIC 3', 5'-CYCLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baehr W., Champagne M.S., Lee A.K., Pittler S.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.8%; Score 183; DB 1; 33.6%; Pred. No. 6.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          858 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27; Mismatches
                                                                                                                                                                                                                    EMBL, L13262; AAA30882.1; ALT_SEQ. PIR; S34290; S34290. InterPro; IPR003018; GAF. InterPro; IPR003018; PDBase_HDc. InterPro; IPR002073; PDBase. InterPro; IPR001230; Prenyl_site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Retina;
MEDLINE=91130581; PubMed=1847109;
                                                                                                                                                                                                                                                                                         Dicerto, ..., Program, Pro1533; PDEase; 1. Pfam; PF01590; GAF; 2. PRINTS, PRO0387; PDIESTERASE1. SMART; SMO065; GAF; 2. SMART; SM00471; HDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    98461 MW;
                                                                                                                                                                                                         EMBL; 223014; CAA80557.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | |:| || ||:
266 AYLNCDRYSVGLLD 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166 TLLKCERCSVLLLE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                            856
853
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853 8
856 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         Disease mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CNRA_MOUSE
P27664;
                                                                              FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                            PROPEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 PFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215 NFVNLIMKVFHLSYLHNCETRRGQILLWSGSKVFEELTDIERQFHKALYTVRAFLNCDRY 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                splicing of the beta-subunit gene.";
FEBS Lett. 278:107-114(1991).
-!- FUNCTION: THIS PROTEIN PARTICIPATES IN PROCESSES OF
TRANSMISSION AND AMPLIFICATION OF THE VISUAL SIGNAL.
-!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)0 =
guanosine 5'-phosphate.
-!- SUBUNIT: OLIGOMER COMPOSED OF TWO CATALYTIC CHAINS (ALPHA AND
BETA), AN INHIBITORY CHAIN (GAMMA) AND THE DELTA CHAIN.
-!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
"Complete cDNA sequences of mouse rod photoreceptor cGMP phosphodiesterase alpha- and beta-subunits, and identification cbeta'-, a putative beta subunit isozyme produced by alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Rod cGMP-specific 3',5'-cyclic phosphodiesterase alpha-subunit
(EC 3.1.4.17) (GMP-PDE alpha).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.8%; Score 183; DB 1; Length 858; ilarity 34.1%; Pred. No. 6.7e-08; Conservative 27; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FARNESYL (BY SIMILARITY).
E29A626B23F7DDA0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00471; HDc; 1.
PROSITE; PS00126; PDEASE_I; 1.
Hydrolase; cGMP; Vision; Prenylation; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             860 AA.
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InterPro; IPR001230; PDEase, 1.9Fam; PP002033; PDEase; 1.9Fam; PF01500; GAF; 2.PRINTS; PR00387; PDIESTERASE1.
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MGD; MGI:97524; Pde6a.
InterPro; IPR003018; GAF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 SVLLLE 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               858 AA;
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Matches 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
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us-09-663-542-1_copy_1_194.rsp

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            YBZJ_CAEEL
P91119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                           C32E12.
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CNRB_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-98099662; PubMed-9233984; Wang W., Acland G.M., Aguirre G.D., Ray K., "Cloning and characterization of the cDNA encoding the alpha-subunit of GGMP-phosphodiesterase in canine retinal rod photoreceptor cells."; Mol. Vision 2:3-3(1996).
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                         Kommonen B., Kylma T., Cohen R.J., Penn J.S., Paulin L., Hurwitz M.,
                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-Beagle X BITISTSUE-RETINE;
STRAIN-Beagle X BITISTSUE-RETINE;
STRAIN-BEAGLE X BITISTSUE-RETINE;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN PARTICIPATES IN PROCESSES OF
TRANSMISSION AND AMPLIFICATION OF THE VISUAL SIGNAL.
-!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)0 =
-!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)0 =
-!- SUBUNIT: OLIGOMER COMPOSED OF TWO CATALYTIC CHAINS (ALPHA AND
BETA), AN INHIBITORY CHAIN (GAMMA) AND THE DELTA CHAIN.
-!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
                                   HURVILZ R.L.; "Elevation of cGMP with normal expression and activity of rod cGMP-PDE in photoreceptor degenerate labrador retrievers."; Ophthalmic Res. 28:19-28(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
FARNESYL (BY SIMILARITY).
M -> L (IN REF. 2).
5260B0BC579A25F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00471; HDc; 1.
PROSITE; PS00126; PDEASE_I; 1.
Hydrolase; cGMP; Vision; Prenylation; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.8%; Score 183; DB.1;
34.1%; Pred. No. 6.7e-08;
ive 27; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003018; GAF.
InterPro; IPR003607; ME_Pplase_HDc.
InterPro; IPR002073; PDEase.
InterPro; IPR001230; Prenyl_site.
           MEDLINE-96331105; PubMed-8726673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam: PF00233; PDE3se; III-2-3
Pfam: PF01590; GAF; 2.
PRINTS: PR00387; PDIESTERASE1.
SMART; SM00055; GAE; 2.
SMART; SM00471; HDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99557 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z68340; CAA92763.1; -. EMBL; U52868; AAB70037.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Y13282; CAA73731.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43; Conservative
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387
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SVGLLD 280
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Best Local Similarity
                                                                                                     SEQUENCE FROM N.A.
 TISSUE-Retina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
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14 RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleoside 5'-phosphate.
SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
FAMILY. STRONG, TO MAMMALIAN TYPE 2 CGMP PHOSPHODIESTERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>ب</u>
                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Probable 3',5'-cyclic phosphodiesterase C32E12.2 (EC 3.1.4.17).
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01-NOV-1991 (Rel. 20, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Rod cGMP-specific 3',5'-cyclic phosphodiesterase beta-subunit PDEGB OR PDEB OR RD OR MPB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Hypothetical protein; Hydrolase; cGMP.
SEOUENCE 393 AA; 44931 MW; 009E4D70297A181C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
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393 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WormPep; C32E12.2; CE08537.
InterPro; IPR003018; GAF.
InterPro; IPR003607; ME_Pplase_HDc.
InterPro; IPR002073; PDEASe.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U80032; AAB53879.1;
WormPep; C32E12.2; CE08537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Pfam; PF01590; GAF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
    STANDARD;
                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00065; GAF; 1
SMART; SM00471; HDC; 1
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AN OCCUPATION OF THE PROPERTY OF THE PROPERTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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PHOSPHODIESTERASE BETA-SUBUNIT.

456 REMANYL-GERANYL (BY SIMILARITY).

856 MISSING (IN ISOFORM 2).

5 G -> E (IN REF. 2).

19 DV -> EL (IN REF. 2).

70 DV -> EL (IN REF. 2).

71 -> P (IN REF. 2).

72 -> L (IN PFF. 3).

73 -> A (IN REF. 3).

74 -> P (IN REF. 3).

75 -> C -> L (IN PFF. 3).

76 -> L (IN PFF. 3).

77 -> P (IN REF. 3).

78 -> EL (IN PFF. 3).

79 -> P (IN PFF. 3).

70 -> P (IN PFF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BETA), AN INHIBITORY CHAIN (GAMMA) AND THE DELTA CHAIN.
SUBCELLULAR LOCATION: Membrane-associated.
ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2/Beta';
are produced by alternative splicing.
DISEASE: DEFECTS IN PDEGB ARE THE CAUSE OF RETINAL DEGENERATION.
SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
                                                                                                                                                                                                                                                                                                                                         Bachr W., Changagne M.S., Lee A.K., Pittler S.J.;
Bachr W., Changagne M.S., Lee A.K., Pittler S.J.;
Complete cDNA sequences of mouse rod photoreceptor cGMP
phosphodiesterase alpha- and beta-subunits, and identification of
beta'. a putative beta-subunit gene.";
Fig. 107-114(1991).
FIRES Lett. 278:107-114(1991).
FIRES Lett. THIS PROTEIN PARTICIPATES IN PROCESSES OF
TRANSMISSION AND AMPLIFICATION OF THE VISUAL SIGNAL. NECESSARY
FOR THE FORMATION OF A FUNCTIONAL PHOSPHODIESTERASE HOLDENZYME.
-:- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)0 =
guanosine 5'-phosphate.
                                                                                                                   "Retinal degeneration in the rd mouse is caused by a defect in the beta subunit of rod cGMP-phosphodiesterase."; Nature 347:677-680(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  guanosine 5'-phosphate.
SUBUNIT: OLIGOMER COMPOSED OF TWO CATALYTIC CHAINS (ALPHA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00126; PDEASE_I; 1.
Hydrolase; cGMP; Vision; Prenylation; Lipoprotein; Membrane;
                                                              , Li T., Danciger M., Baxter L.C., Applebury M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G -> E (IN REF. 2).

DV -> EL (IN REF. 2).

T -> P (IN REF. 2).

C -> L (IN REF. 2).

C -> L (IN REF. 2).

S -> E (IN REF. 2).
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InterPro; IRR003018; GAF.
InterPro; IPR003607; ME_Pplase_HDc.
InterPro; IPR002073; PDEase.
InterPro; IPR001230; Prenyl_site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X55968; CAA39439.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                    TISSUE=Retina;
MEDLINE=91130581; PubMed=1847109;
STRAIN=C57BL/6; TISSUE=Retina;
MEDLINE=91015387; PubMed=1977087;
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Pfam; PF01500; GAF; 2.
PRINTS: PR00387; PDIESTERASE1.
SMART; SM00065; GAF; 2.
SMART; SM00471; HDC; 1.
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                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Gaps

5

64; Indels

Query Match 17.9%; Score 175; DB 1; Best Local Similarity 33.6%; Pred. No. 3.1e-07; Matches 45; Conservative 23; Mismatches 64,

Length 856;

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148 MINVQDVAECTHFSSFADELTDYVTKNICSTPIMNGK-DVVAVIMAVNKL-DGPCFTSED 205
                                      106 EKVMQMYLPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQ 165
                                                          Search completed: June 13, 2003, 15:47:44
Job time : 5.97722 secs
                                                                                                           166 TLLKCERCSVLLLE 179
                                                                                                                                qq
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                                                                                                         Qγ
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46 LIQRQTKTKDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDD 105

155.4 7.5 884 150.8 7.3 719 150.8 7.3 941 142.8 6.9 401 142.8 6.9 744 140.4 6.8 583 140.4 6.8 591 138.2 6.7 639	137.8 6.6 1067 13 BM450793 135.8 6.5 875 14 B0926876 135.8 6.5 561 10 BE107807 132.8 6.4 905 17 CNS01E4X 130.2 6.3 800 12 BG214519 128.8 6.2 747 12 BG342646 127.2 6.1 876 13 B1733977 126.8 6.1 790 12 BG206143 124.4 5.9 516 12 BG087768	121.8 5.9 636 14 BM950937 121.8 5.9 636 14 BM950937 121 5.8 747 12 BG171485 119.8 5.8 747 12 BG15073 119.8 5.8 747 12 BG215073 119.6 5.8 632 13 B1285696 119.2 5.7 782 9 AU120086 118.2 5.7 579 13 B1305168 117.6 5.7 621 13 B1305168		ALIGNMENTS	RESULT 1 BB595063 LOCUS BB595063 DEFINITION BB595063 RIKEN full-length enriched, adult male corpus striatum Mus musculus CDNA clone C030004B19 5', mRNA sequence. ACCESSION BB595063.2 GI:16450156 KEYWORDS EST ONGANISM Mus musculus CONGRE ORGANISM Mus musculus REFERENCE I (basezoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. REFERENCE I (bases I to 648)	
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd. leic search, using sw model June 20, 2003, 15:05:11; Search time 3005 Seconds (without alignments) 11199,408 Million cell updates/sec	US-09-663-542-2 2078 1 ggtccgagatgctgaagcagactaataactcgaggcatgc 2078 IDENTITY_NUC Gapop 10.0 , Gapext 1.0 16154066 seqs, 8097743376 residues	Lifying chosen par 000000000 Match 0% Match 100% first 45 summarie	F:* em_estba:* em_esthum:* em_estin:* em_estin:* em_estov:* em_estpl:* em_estpl:* em_estpl:* em_estpl:* gb_est1:*	1: gp_ntc:* 2: gb_est3:* 3: gb_est4:* 4: gb_cst4:*	14: 9J_est.): 16: em_estun:* 17: 9J_est.: 18: em_estun:* 18: em_gss_hum:* 19: em_gss_pln:* 20: em_gss_pln:* 21: em_gss_pln:* 22: em_gss_pln:* 23: em_gss_nun:* 24: em_gss_other:* 25: em_gss_other:* 26: em_gss_other:* 27: em_gss_rod:*	No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution. SUMMARIES Query Ratch Length DB ID 28 25.4 648 10 BB55063 73 22.8 724 10 BB639291 8 10.4 459 12 B6554930 10.4 459 12 B6554930 10.8 89 501 13 B1672945 10.8 89 501 13 B1672945 10.8 80 472 17 A0312583 10.4 872 17 A0312583 10.4 872 17 A0312583 10.4 8.0 472 17 A0312583
Co OM nucleic - nucleic Run on: June	Title: Perfect score: 20 Sequence: 1 Scoring table: ID Searched: 16	mber of h DB seq le DB seq le cessing:	Database : 1: 2: 2: 3: 3: 4: 4: 4: 4: 4: 4: 4: 4: 4: 4: 4: 4: 4:			Pred. No. is the score greater and is derived and is derived No. Score Matc. No. Score Matc. 1 528 25. 2 473 22. 3 216.8 10. 4 184.8 8. 5 5 177 8.

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Dukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bass. 1 to 724)

Arakawa.T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramotto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, H., Kouda, C., Sakai, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takabashi, F., Takeda, Y., Tanaka, T., Toya, T., RIKEN Mouse, ESTS (Arakawa, T., et al. 2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BB639291 RIKEN full-length enriched, 3 days neonate thymus Mus musculus cDNA clone A630086N24 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-ho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
                        GCTGCCTCAAGGAAAGAATACGAAAGAAGCAGGCCCTGCTGGAGGTGGTGGTCAATGACCTC 180
                                                                                                                                                                                                                                                                        541 ATTIGGAACAGCAACCACCAAATAATIGGGGTGGCTTAAGTGTTGAACAGAACTCACCGA 600
AAAGTTATGCAGATGTATCTTCCATTTTGTGGAATCGCCATATCTAACGCTCAGCTCTTT
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                                                                                         GCTGCCTCAAGGAAAGAATATGAAAGAAGCAGAGCTTTGCTAGAGGTGGTTAATGACCTC
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Contact: Yoshihide Hayashizaki
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Nondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
Hayashizaki,Y.
                                                                                                                                                                                                                                                                    RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 175-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
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URL:http://genome.go.gr.riken.go.jp,
Carninci.p., Shibata,Y., Haytawa.N., Sugahara,Y., Shibata,K., Itoh
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Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
penere. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="C030004B19"
/clone_lib="RIKEN full-length enriched, adult male corpus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Site_1: Sall; Site_2: BamHI: cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKBN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3']. cDNA was cloned into the XhoI and BamHI sites.
Vector: a modified pBluescript KS(+) after bulk excision
from Lambda FLC I. Cloning sites, 5' end: Sall; 3' end:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA library was prepared and sequenced in Mouse Genome broyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Computational Analysis of Full-Length Mouse cDNAs Compared with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 GGTGTGGCCCAAGCGATAAATAAGATTCCTGAAGGAGCTCCATTTACTGAAGATGAA
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Pred. No. 1e-141;
); Mismatches 75;
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/dev_stage="adult"
/lab_host="DH10B"
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FEATURES

Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh

Query Match Best Local S

Matches

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BASE COUNT

ORIGIN

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626 360 989 420 806 540

702

us-09-663-542-2.rst

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1 (bases 1 to 459)
Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D., Martin, J., Wylle, T., Underwood, K., Theising, B., Bowers, Y., Person, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: estëwatson.wustl.edu
Library constructed by Life Technologies. DNA Sequencing by:
Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Conscrtium/LLNL at: info@image.llnl.gov
Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST 09-APR-2001
                                                      362 CAGGCCTTCCTGTGAATGTCAGCGATGCCTACCAGGACCCACGCTTTGACGCTGAGGCTG 421
                                                                                                                                                                                                                                                                                                                                             ACCAAATAATTGGAGTGGCTCAAGTGTTAAACAGACTTGATGGGAAACCTTTTGATGATG 882
                                                                                                                                                                                                                                                                                                                                                                                                                                         dac34a09.y1 NICHD XGC Hel Xenopus laevis cDNA clone IMAGE:4408625
5' similar to TR:Q9VJ79 Q9VJ79 CG10231 PROTEIN. ;, mRNA sequence.
BG554930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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/note="Organ: heart; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT,
Average insert size 1.6 kb. Constructed by Life
                                                                                                                                                                                                                          CAGGCCTTCCAGTGAACATCAGTGATGCCTACCAGGATCCGCGCTTTGATGCAGAGGCAG
                                                                                                                                                                                                                                                                                                                       ACCAGATATCTGGTTTTCACATAAGATCTGTTTTTTGTGTCCCTATTTGGAATAGCAACC
                                AGAAATCATCATACTCCGACTGGCTAATAAATAACAGCATTGCTGAGCTGGTTGCTTCAA
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
7Fel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                              /db_xref="taxon:8355"
/clone="IMAGE:4408625"
/clone_lib="NICHD xGC Hel"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WashU Xenopus EST project, 1999
Unpublished (1999)
Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
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                                                                                                                                                                                                                                                                                                                                        encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa H., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
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,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rappid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
'S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
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GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTVN 3'], cDNA was
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                                                                                                                                                                                                                                                                                                                                                                                                                                                haydsultaki,i.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.rlken.go.jp) for
further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10; Length 724;
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Pred. No. 1e-125;
0; Mismatches 5
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/lab_host="DH10B"
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/clone="A630086N24"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ft39412.y1 Gong zebrafish testis Danio rerio cDNA clone 5153110 5/
similar to TR:Q9VJ79 Q9VJ79 CG10231 PROTEIN. ;, mRNA sequence.
B1672945
B1672945.1 G1:15588329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l (bases 1 to 501)
Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S.L., Hiller, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
                                      ö
                                                                         1690 TAATGACAGCCTGTGACCTTGGAGCCGTGACCAAACCGTGGGAGATCTCCAGACAGGTGG 1749
                                                                                                                                                1750 CAGAACTTGTAACCAGTGAGTTCTTCGAACAAGGAGATCGGGAGAGATTAGAGCTCAAAC 1809
                                                                                                                                                                                                                        1810 TCACTCCTTCAGCAATTTTTGATCGGAACCGGAAGGATGAACTGCCTCGGTTGCAACTGG 1869
                                                                                                                                                                                                                                                                                               1870 AGTGGATTGATAGCATCTGCATGCCTTTGTATCAGGCACTGGTGAAGGTCAACGTGAAAC 1929
                                                                                                                                                                                                                                                                                                                                                                        TGAAGCCGATGCTAGATTCAGTAGCTACAAACAGAAGTAGTGGGAAGAGCTACACCAAA 1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: zbrafish@watson.wustl.edu
The library was constructed by Dr. Z. Gong. DNA Sequencing by:
Mashington University Genome Sequencing Center St. Louis. Please
contact Zhiyuan Gong for further information on this library
(National University of Singapore, Department of Biological
Sciences, Lower Kent Ridge Road, Singapore 119260).
                                                                                            1 TAATGACAGCGTGTGAGACCTTGGAGCTGCAACCAAACCATGGGAGATTTCCAGACAGGGGG
                                                                                                                                                                  181 AATGGATTGACAACATTTGTTTTCCTTTATATGAGTCGCTAGTCAAGATCAGTGGAAAGC
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1998)
Other_ESTS: ft39412.x1
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fal: 314 286 1800
Fax: 314 286 1810
                                      ;
0
   Length 459;
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                1990 AACGACTGCTGGCCTCAACTGCCTCATCCTCCCCCTGC 2029
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/sex="male"
                     2.1e-51;
                                                                                                                                                                                                                                                                                                                    0; Mismatches
 Score 216.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WashU Zebrafish EST Project 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Danio rerio"
                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: T3 ET from Amersham
High quality sequence stop: 393.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="4-5 month"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:7955"
/clone="5153110"
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10.4%;
                                      Conservative
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                   Similarity
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                                    263;
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 Query Match
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                     Best Loca
Matches
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JOURNAL
COMMENT
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.BI672945
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KEYWORDS
SOURCE
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/lab_host="DH10B (phage-resistant)"
//note="Organ: testis (poolded): Vector: pBluescript SK-:
Site_1: XhoI: Site_2: EcoRI: Poly A+ RNA was isolatd from
the testes of 31 male adult zebrafish (4-5 month old).
CDNAs were made using oligo-dT primers and inserted into
lambda ZAP II vector (Stratagone) by Dr. Z. Gong, in vivo
mass-excised to pBluescript SK- following the Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BQ014209 689 bp mRNA linear EST 26-MAR-2002
UI-H-EDI-axs-k-16-0-UI.s1 NCT_CGAP_ED1 Homo sapiens cDNA clone
IMAGE:5833095 3′, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1890 ATGCCTTTGTATCAGGCACTGGTGAAGGTCAACGTGAAACTGAAGCCGATGCTAGATTCA 1949
                                                                                                                                                                                                                                  (http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Zhiyuan Gong for further information on this library (National University of Singapore,
Department of Biological Sciences, Lower Kent Ridge Road,
Singapore 119260)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 GGTGCAGTGACTCGACCATGGGAGATCTCAAAACAGGTGGCTGAACTGGTGACCAGTGAA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi, Mammallai; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 689)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1650 TGGAACATCAAAAACCATCGTGATATATTTCGATCAATGTTAATGACAGCCTGTGACCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 184.8; DB 13;
Pred. No. 4.3e-42;
); Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1950 GTAGCTACAAACAGAAGTAAGTGGGAAGAGCT 1981
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       308 ATTGATGCCAACCGAAGAAGAAGTGGGAGGAGCT 339
                                                                                                                                                                                                                                                                                                                                                                                   106 t
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Unpublished (1997)
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884 bp mRNA linear EST 12-JUL-2000 5' MRNA sequence.
AUO79253 SUGATION MOS MUS MUSCULUS CDNA CLONE MNCD-4049 AUO79253 I GI:6084008
                                         AQ312583
AQ111-95E23.TJ RPCI-11 Homo sapiens genomic_clone RPCI-11-95E23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                           1 (bases 1 to 472)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.
Use of human BAC End Sequences for Sequence-Ready Map Building
Unpublished (1998)
Other_GSSs: RPCIII-95E23.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 AAAAAGGTGAAAATCACAAGACTGGTCCAAATCTCTGGGGCCTCTTTGGCTGAAAAACAG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 AAAAAGGTGAAAATCACAAAACTGGTCCAAATCTCTGGGGCCTCTTTGGCTGAAAAACG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html Seq primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92
                                                                                                                                                                                                                      Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: ECORI; Site_2: ECORI;
RPCIII Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 GAGATGCTGAAGCAGGCAAGAAGACCTTTATTCAGAAATGTGCTCAGTGCCACACAGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGATGCTGAAGCAGGCAAGAAGACCTTTATTCAGAAATGTGCTCAGTGCCACACAGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                             Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Pred. No. 1.2e-36;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
/clone="RPCI-11-95E23"
/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="GDB:7536214"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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100.0%; Pre
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                                                                                      DNA sequence.
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Best Local Similarity
Matches 166; Conserv
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house mouse.
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AQ312583.1
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                                                                                                                                                                             human.
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COMMENT
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VERSION
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AUTHORS
                                                                                                         ACCESSION
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SOURCE
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AU079253
RESULT 6
AQ312583
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                                                                                                                                                                /note="Organ: Left Public Bone; Vector: pT713-Pac
(Pharmacia) with a modified polylinker; Site_1: Ecor I;
Site_2: Not I: NoT_CGAP_EDI is a normalized cDNA library
containing the following tissue(s): Chondrosarcoma cell
line CSS. The library was constructed according to Bonal
o' Lennon and Soares, Genome Research, 6:91-806, 1996.
First strand cDNA synthesis was primed with an oligo-
ptimer containing a Not I site. Double stranded cDNA was
ligated to an EcoR I adaptor, digested with Not I, and
cloned directionally into pT772-per vector. The
oligonuclectide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GCTCAAGGCT.
TAG_LIB-UI-H-EDI
TAG_LIB-UI-H-EDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGATGATCCTTCAAAGTGAGGGTCACAATATCTTTGCTAACCTGTCCTCCAAGGAATAT 1541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1362 CTGTGTCATGACCTCGACCACAGGGGAACCAACAATGCCTTCCAAGCTAAGAGTGGCTCT 1421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCCTGGCCCAACTCTATGGAACCTCTGCTACCTTGGAGCATCACCATTTCAACCACGCC 1481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGTGACCTTATGCAGCTTTTGAAGCAGTCAATATTGGCAACAGACCTCACGCTGTACTTT 1601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGGATGAACTGCCTCGGTTGCAACTGGAGTGGATTGATAGCATCTGCATGCCTTTGTAT 1901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1662 AACCATCGTGATATATTCGATCAAGGTAATGACAGCCTGTGACCTTGGAGCCGTGACC 1721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAACCGTGGGAGATCTCCAGACAGGTGGCAGAACTTGTAACCAGTGAGTTCTTCGAACAA 1781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         624 CCACTTGCCCAGCTTTACTG---CCATTCAATCATGGAACACCATCATTTGACCAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGACCACGTTGAAAATAATCAAGCAAGCTATTTTAGCTACAGACCTAGCACGTGGACAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                387 CATCAAAAGGAGTTGTTTTTGGCAATGCTGATGACAGCTTGTGTATCTTCTGCAATTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    567 CTGATGATTCTTAATAGTCCAGGCAATCAGATTCTCAGTGGCCTCTCCATTGAAGAATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.5%; Score 177; DB 14; Length 689; 58.8%; Pred. No. 9.6e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                             /clone_lib="NCI_CGAP_ED1"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH108 (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ىد
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                  /organism="Homo sapiens'
/db_xref="taxon:9606"
                                                           /clone="IMAGE:5833095"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAG_SEQ=CGTCAAGGCT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 Similarity 322; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182
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source
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BI259167.1 GI:14816236
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ORIGIN
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AUTHORS
TITLE
JOURNAL
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            //occ="Oconic brain; Vector: pME18S-FL3; 1st strand cDNA was primed with an oligo(dT) primer ATGTGGCCTTTTTTTT]; double-stranded cDNA was ligated to a DraII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3. XhoI sites just outside the DraIII sites can be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5 kb. Library was constructed by Sugano et al. (University of Tokyo, Institute of Medical Science). Custon primer used for sequencing: 5' end primer [CTTCTGCTCTAAAAGCTGG], 3' end primer [CGACCTGCAGCAGG], 3' end primer [CGACCTGCAGCAGA]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1231 ATCGGATGGTTCTATACCACAACTGGAGACATGCCTTCAACGTGTGTCAGCTGATGTTCG 1290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1291 CGATGTTAACCACTGCTGGGTTTCAAGACATTCTGACGAGGTGGAAATTTTAGCGGTGA 1350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1351 TTGTGGGATGCCTGTGTCATGACCTCGACCAGGGGAACCAACAATGCCTTCCAAGCTA 1410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1411 AGAGTGGCTCTGCCCTGGCCCAACTCTATGGAACCTCTG---CTACCTTGGAGCATCACC 1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1468 ATTTCAACCACGCCGTGATGATCCTTCAAAGTGAGGGTCACAATATCTTTGCTAACCTGT 1527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTCCAAGGAATATAGTGACCTTATGCAGCTTTTGAAGCAGTCAATATTGGCAACAGACC 1587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1588 TCACGCTGTACTTTGAGAGGAGAACTGAATTCTTTGAACTTGTCAGTAAAGGAGAATACG 1647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 TGCTCTACAAGAATCTGGAGCTCTCCAACTACCTCGAGACATCGAGATCTTTGCATTGT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 CCTCGAAATCTGTGCTGGCGCGCACTCTACAGGGGCTCTGTCATGGAGGGCACC 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCGGAAGGACTATCAGCGCATGCTGGACCTGATGAGGGACATCATCTTGGCTACAGACC 422
                                                                 Hashimoto, K., Kusuda, J., Tanuma, R., Ito, A., Hirata, M., Toyoda, A., Suzuki, Y., Sasaki, M. and Sugano, S.
Suzuki, Y., Sasaki, M. and Sugano, S.
Isolation of full-length cDNA clones from a mouse brain cDNA
library made by oligo-capping method
Unpublished (1999)
Unpublished (1999)
Contact: Katsuyuki Hashimoto
Division of Genetic Resources
National Institute of Infectious Diseases
National Institute of Infectious Diseases
33-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
Email: Khashi@nih.go.jp
URL: http://www.nih.go.jp/yoken/genbank/.
                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 884)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1171 AGAAATTTAAAATTGACTATGAGACACTGTGTAGGTGGCTTTTGACAGTGAGGAAAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATAACANCAAAATTGACTGCCCAACTCTGGCCCGATTCTGCCTGATGGTGAAGGAAAGGCT
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9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Sugano mouse brain mncb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 155.4; DB 9;
Pred. No. 2.1e-33;
0; Mismatches 277;
                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="adult"
/lab_host="TOP10"
                                                                                                                                                                                                                                                                                                                                                                         /clone="MNCb-4049"
                                                                                                                                                                                                                                                                                                                                  'strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                            /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.5%;
54.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    344; Conservative
                                                                                                                                                                                                                                                                                            .884
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Matches 34
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ORGANISM
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ORIGIN
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                                                    REFERENCE
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1200 TGTAGGTGGCTŤTTGACAGTGAGGAAAAACTATCGGATGGTTCTATACCACAACTGGAGA 1259~
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                                                                                ATTGGAACATCAAAAACCATGGTGATATATTTGGATCAATGTTAATGACAGCCTGTGACC 1707
                                                                                                                                                                                          TTGGAGCCGTGACCAAACCGTGGGAGATCTCCAGACAGGTGGCAGAACTTGTAACCAGTG 1767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BI259167 719 bp mRNA linear EST 17-JUL-2001 602970010F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5109435 5',
GCCCGGTTCTGTTTGATGGTGAAGAGGCTACCGGGATCCCCCCTACCACAACTGGATG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Library prepared by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                     ACCGAAACAACAGGCAACACCACAGGCTTCTTCTGNGCCTCCTCATGACCTCCTGNGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1260 CATGCCTTCAACGTGTGTCAGCTGATGTTCGCGATGTTAACCACTGCTGGGTTTCAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1140 CTCCGGATGTTCATGGAGCTGGGATGGTACAGAAATTTAAAATTGACTATGAGACACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 719)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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Pred. No. 4e-32;
0; Mismatches 297; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="InAGE:5109435"
/clone_lib="NIH_MGC_12"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nin.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, In
CDNA Library Arrayed by: Incyte Genomics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plate: LLAM11265 row: c column: 04
High quality sequence stop: 715.
Location/Qualifiers
1. 719
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Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI025081 401 bp mRNA linear EST 27-AUG-1998 ov40all.xl Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1639772 3' similar to TR:028156 Q28156 CGMP-SPECIFIC PHOSPHODIESTERASE. ;, mRNA sequence.

AI025081.1 GI:3240694
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                                                                                                                                                     1140 CTCCGGATGTTCATGGAGCTGGGGATGGTACAGAAATTTAAAATTGACTATGAGACACTG 1199
                                                                                                                                                                                                                                                                                                                                                                                                                 1320 ATTCTGACCGAGGTGGAAATTTTAGCGGTGATTGTGGGATGCCTGTGTCATGACCTCGAC 1379
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Kakaryota: Metazoa; Chordata: Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                CTGAGCATGCTGCAGGACATGAATTTCATCAACAACTACAAAATTGACTGCCCGACCCTG
                                                                                                            Gaps
                                                                                                            9
                                                               Length 941;
                                                                                                          0; Mismatches 297; Indels
                                                                 DB 13;
                                                                                        Pred. No. 4.7e-32;
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                                                                                                                                                                                                                     304 AGCTCTGAGGGCTCCGTCATGGAGGCACCACTTTGCTCAGGCCATCGCCATCCTCAAC 363
                                                                                                                                                                                                                                                                                                           ACCCACGCCTGCAACATCTTTGATCATTTCTCCCGGAAGGACTATCAGCGCATGCTGGAT 423
                                                                                                                                                   /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT Average insert size 1.4 kb. Library prepared by Life Technologies.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 941)
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CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM11265 row: b column: 04
High quality sequence stop: 771.
                      ATTCTGACCGAGGTGGAAATTTTAGCGGTGATTGTGGGATGCCTGTGTCATGACCTCGAC
                                             CACAGGGGAACCAACAATGCCTTCCAAGCTAAGAGTGGCTCTGCCCTGGCCCAACTCTAT
                                                                                                                                                                                                                                                                                                                                                                                                 NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/db_xref="taxon:9606"
/clone="Indege:5109411"
/clone_lib="NIH_MGC_12"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
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/ dev_stage="minton" is to dev_stage="minton" is dev_stage="minton
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                                                                                                                                                                                                                                                                                                /tissue_type="whole brain"
                                                                                                                                                                                                                                                           clone_lib="NIH_BMAP_EVO"
                                                                                                                           /organism="Mus musculus"
                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="IMAGE:5707914"
                                                                   Location/Qualifiers
                                                                                                                                                                /strain="C57BL/6"
                                    pYX-5
                                 Seq primer:
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(BMAP)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories
                                                               Sequencing Center
information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. James Lih, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sciurognathi, Muridae; Murinae; Mus
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 744)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGAAAATTGTCAAGAAAATAATGCATCGGGCCCAAACTCTGCTGAAATGTGAGCGCTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               409 AAAGAAGCAGAGCTTTGCTAGAGGTGGTTAATGACCTCTTTGAAGAACAGACTGACCTGG
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IMAGE:5707914 5', mRNA sequence.
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                       cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consorttum/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 144.4; DB 9;
Pred. No. 2e-30;
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                                                                                                                                                   www-bio.lln1.gov/bbrp/image/image.html
Insert Length: 648 Std Error: 0.00
Seg primer: -40ml3 fwd. ET from Amersham
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                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9666"
/clone="IMAGE:1639772"
/clone_lib="Soares_testis_NHT"
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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Cenome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTC 19-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                         1652 GAACATCAAAAACCATCGTGATATATTTCGATCAATGTTAATGACAGCCTGTGACCTTGG 1711
                                                                                                                                                                              1532 CAAGGAATATAGTGACCTTATGCAGCTTTTGAAGCAGTCAATATTGGCAACAGACCTCAC 1591
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Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:1700008G06:cytochrome c, testis, full insert
302 GAAATCTGTGCTGGCTGCGCTCTACAGCTCTGAGGGCTCCGTCATGGAGGGCACCACTT
                                                                                                                                                                                                                                                                                      1592 GCTGTACTTTGAGAGGAGAACTGAATTCTTTGAACTTGTCAGTAAAGGAGAATACGATTG
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                                                                                                                           362 recreaegecarecearecreaegecaegergeaacarerrrgarearrrerece
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                                                                                                                                                                                                                                                                                                                                                                                                                                      539 AAACAACAAGCAGCACCACAGACTTCTCCTCTGCCTCCTCATGACCTCCTGTGACCTCTC
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AKO18833.1 GI:12858775
HTC; CAP trapper.
Mus musculus (strain:C57BL/6J) adult male testis cDNA to mRNA,
clone_lib:RIKEN full-length enriched mouse cDNA library
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT Average insert size 1.4 kb. Library prepared by Life
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I thoses 1 to 644)

NHH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can http://mage.lnh.gov
Plate: LimM11298 row: n column: 19
                        GACCTTGGAGCCGTGACCAAACCGTGGGAGATCTCCCAGACAGGTGGCAGAACT 1756
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/clone=lnb="NH_NOC_12"
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Pred. No. 2.6e-29;
0; Mismatches 295; Indels
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Location/Qualifiers
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205 c
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53.3%;
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                                                                                                                                                                                                                                                        mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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us-09-663-542-2.rst

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTC 19-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Fujiwake, S., Matumoto, H., Togawa, Y., Izawa, M., Ohara, E., Matahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawi, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AK005582 591 bp mRNA linear HTC 19-JAN-2
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:1700001D24:cytochrome c, testis, full insert
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AK005582.1 GI:12838235
HTC: CAP trapper.
Mus musculus (strain:C57BL/6J) adult male testis CDNA to mRNA,
clone_lib:RIKEN full-length enriched mouse cDNA library
clone:1700001D24.
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Pred. No. 3.7e-29;
); Mismatches 16;
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                            /gene="Cyct"
/note="putative"
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             /codon_start+1
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Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G.,
Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M.,
Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojungan, N.,
Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,
Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H.,
Toyo-oka, K., Wang, K.H., Weitz, C., Willming, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission Submitted (18-MG-2000) Yoshihide Hayashizaki, The Institute of Submitted (18-MG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Tokohama Institute: 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-resegsc:riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9216)
Pleasse visit ur web site (http://genome.gsc.riken.go.jp/) for firther details.
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1. .583
                                                                                                                                                                                                                                                                                            Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
                                                                                                                                                                                                                                                                                                                 and Hayashizaki,Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
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        /clone_lib="RIKEN full-length enriched mouse cDNA library"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AK018851 591 bp mRNA linear HTC 19-JAN-2
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:1700048D19:cytochrome c, testis, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 GAGATGCTGAAGCAGCAAGAAGACCTTTATTCAGAAATGTGCTCAGTGCCACACAGTGG
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AK018851.1 GI:12858802
AK018851.1 GI:12858802
Mus musculus (strain:C57BL/6J) adult male testis cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:1700048D19.
                                                                                                                                                                     /note="cytochrome c, testis
data source:MGD, source key:MGI:88579, evidence:ISS
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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/db_xref="GI:12838236"
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                               /dev_stage="adult"
1. .591
                                                                                                                                                                /note="cytochrome
                                                                                                                                                                                                                                                     /codon_start=1
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Best Local Similarity 90.4%;
Matches 150; Conservative
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                                                                                                                                            /gene="Cyct"
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AK018851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanaqawa 230-0045, Japan (E-mail:genome-res@sc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)
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/tissue_type="testis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5, GAGAGAGAGAGACCCTTTTTTTTTTTTTTTTVN 3/1, cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukudishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J. Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Sofrimi, L., Shibata, K., Shibata, Y., Shinaqawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Tagawa, A., Tagawa, A., Tagawa, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)
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Adachi, J., Aizawa, K.
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/organism="Mus musculus"

source

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1. 591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 AAAAAGGTGAAAATCACAAGACTGGTCCAAATCTCTGGGGCCTCTTTGGCTGAAAAACAG 125
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/clone="1700048D19"
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Human phosphodiest Human phosphodiest

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Cyclic guanosine m Bovine phosphodies

Human cGB-PDE cDNA

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Bovine brain cGS-P cGS-PDE cDNA isola Bovine brain cGS-P cGS-PDE cDNA clone

Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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Human, cyclic nucleotide phosphodiesterase; PDEXV; sexual dysfunction; cardiovascular disease; gastrointestinal disorder; corpus cavernosum; kidney; liver; skeletal muscle; testis prostate; spleen; ss.
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                             The present invention describes the protein and coding sequences of the human cyclic nucleotide phosphodiesterase PDEXV. This enzyme is capable of catalysing the degradation of cyclic nucleotides. The sequences are useful in the treatment of cardiovascular, gastrointestinal, spleen, corpus cavernosum, kidney, liver, skeletal muscle, testis and prostate related disorders, and in the enhancement of the male erectile response and the treatment of female sexual dysfunction. The present sequence is
                                                                      Human cyclic nucleotide phosphodiesterase and its nucleotide sequence useful for treating cardiovascular disorders, sexual dysfunction and screening for drugs to treat associated disorders -
                                                                                                                                                                                                                                                                                                                                                                                              GGTCCGAGATGCTGAAGCAGGCAAGAAGACCTTTATTCAGAAATGTGCTCAGTGCCACAC
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                                                                                                                                    Claim 3; Page 42-43; 44pp; English
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Matches 2078; Conservative
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180 240 240 480 099 120 180 300 300 360 360 420 420 540 540 900 AGTGGAAAAAGGTGAAAATCACAAGACTGGTCCAAATCTCTGGGGCCTCTTTGGCTGAAA 120 099 ACTGGCTAATAAATAACAGCATTGCTGAGCTGGTTGCTTCAACAGGCCTTCCAGTGAACA 720 TCAATGATGAAATCGACAAGCTGACTGGATACAAGACAAAATCATTATTGTGCATGCCTA GAGCTCCATTTACTGAAGATGAAAAAAGTTATGCAGATGTATCTTCCATTTTGTGGAA TCGCCATATCTAACGCTCAGCTCTTTGCTGCCTCAAGGAAAGAATATGAAAGAAGCAGAG CTTTGCTAGAGGTGGTTAATGACCTCTTTGAAGAACAGACTGACCTGGAGAAAATTGTCA AGAAAATAATGCATCGGGCCCAAACTCTGCTGAAATGTGAGCGCTGTTCTGTTTTACTCC AGAAAATAATGCATCGGGCCCAAACTCTGCTGAAATGTGAGCGCTGTTCTGTTTTACTCC TAGAGGACATCGAATCACCAGTGGTGAAATTTACCAAATCCTTTGAATTGATGTCCCCAA AGTGCAGTGCTGATGCTGAGAACAGTTTCAAAGAAAGCATGGAGAAATCATACTCCG 61 61 121 181 181 241 241 301 301 361 361 421 481 541 541 601 601 121 421 481 661 661 à g ò g οy Ор οy q Qγ Ω ò Dp δλ d QΫ́ g ò qq ŏ g ò

Qy.	721	TCAGTGATGCCTACCAGGATCCGCGCTTTGATGCAGAGGCAGACCAGATATCTGGTTTTC 780 #C11
ga	7	RGIGAIGCCIACCAGGAICCGCGGTTIGAIGCAGAGGCAGACCAGAIAICIGGTTTIC /8
δy	781	GTCCCTATTTGGAATAGCAACCACCAAATAATTGGAGTGG 84
Db	781	ATAAGATCTGTTCTTTGTGTCCCTATTTGGAATAGCAACCACCAAATAATTGGAGTGG 84
δλ	4	GATGGGAAACCTTTTGATGATGCAGATCAACGACTTTTTG 90
QQ	841	CAAGTGTTAAACAGACTTGATGGGAAACCTTTTGATGATGCAGGATCAACGACTTTTTG 90
Qy	901	GTCATCTTTTGTGGACTTGGCATCAACACACAATTATGTATG
QQ	901	SCTTTTGTCATCTTTTGTGGACTTGGCATCAACAACACAATTATGTATG
٥y	961	CTGGGCCAAGCAGTCTGTGGCTCTTGATGTGCTATCATACCATGCAACATGTT 1
Db	961	AGTCCTGGGCCAAGCAGTCTGTGGCTCTTGATGTGCTATCATACCATGCAA
Qy	1021	SCTGAAGTTGACAAGTTTAAGGCAGCCAACATCCCTCTGGTGTCAGAACTTGCCA
Db	1021	AAAAGCTGAAGTTGACAAGTTTAAGGCCAGCCAACATCCCTCTGGTGTCAGAACTTGCCA
Qy	1081	ATTCATTTTGATGACTTTTCTCTCGACGTTGATGCCATGATCACAGCTGCTC
Db	1081	CGATGACATTCATTTTGATGACTTTTCTCTCGACGTTGATGCCATGATCACAGCTGCTC 114
Qy	1141	TCATGGAGCTGGGGATGGTACAGAAATTTAAAATTGACTATGAGACACTGT
QQ	1141	CCGGATGTTCATGGAGCTGGGGGATGGTACTTTAAAAATTGACTATGAGACACTCT
Οy	1201	GGCTTTTGACAGTGAGGAAAAACTATCGGATGGTTCT
Dp	1201	TAGGTGGCTTTTGACAGTGAGGAAAAACTATCGGATGGTTCTATACCACAACTGGAGAC 126
Οy	1261	TGCCTTCAACGTGTCAGCTGATGTTCGCGATGTTAACCACTGCTGGGTTTCAAGACA
QQ	1261	CCTTCAACGTGTGTCAGCTGATGTTCGCGATGTTAACCACTGCTGGGTTTCAAGACA 132
Qy	1321	ICTGACCGAGGTGGAAATTTTAGCGGTGATTGTGGGGATGCCTGTGTCATGACCTCGACC 138
QQ	1321	CTGACCGAGGTGGAAATTTTAGCGGTGATTGTGGGATGCCTGTGTCATGACCTCGACC 138
Qy	1381	AAGTGCTCTGCCCTGGCCCAACTCTATG 144
qq	1381	CAGGGGAACCAACAATGCCTTCCAAGCTAAGAGTGGCTCTGCCCTGGCCCAACTCTATG 144
·Qy	4	TACCTTGGAGCATCACCATTTCAACCACGCCGTGATGATCCTTCAAAGTG 150
Db	1441	AACCICIGCTACCTIGGAGCAICACCATITCAACCAGGCCGTGATGATCTTCAAAGTG 150
Qy	1501	CACAATATCTTTGCTAACCTGTCCTCCAAGGAATATAGTGACCTTATGCAGCTTT
qa	1501	GGGTCACAATATCTTTGCTAACCTGTCCTCCAAGGAATATAGTGACCTTATGCAGCTTT
Qy	1561	CAGTCAATATTGGCAACAGACCTCACGCTGTACTTTGAGAGGAGAACTGAATTCT 1
qq	1561	GAAGCAGTCAATATTGGCAACAGACCTCACGCTGTACTTTGAGAGGAGAACTGAATTCT 16
Qy	1621	THE STATE OF THE S
qq	1621	TGAACTTGTCAGTAAAGGAGAATACGATTGGAACATCAAAAACCATCGTGATATTTC 168
Qγ	1681	CAATGTTAATGACAGCCTGTGACCTTGGAGCCGTGACCAAACCGTGGGAGATCTCCA 1
. da	1681	ATCAATGTTAATGACAGCCTGTGACCTTGGAGCCGTGACCGTGGGGGATCTCCA 174
ΟY	1741	CAGAACTTGTAACCAGTGAGTTCTTCCAACAAGGAGATCGGGAGAGATTAG
Dþ	1741	ACAGGTGGCCAGAACTTGTAACCAGTGAGTTCTTCGAACAAGGAGATCGGGAGAGTTAG 18

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                                         The present invention provides the protein and coding sequences of novel human and rat type 11 phosphodiesterases (PDEII). These are useful for studying intracellular signal transduction mechanisms, in screening highly-selective inhibitors as drugs for treating diseases associated with the enzymes and for the identification or selection of selective inhibitory action against multiple type phosphodiesterases. The present sequence is a coding sequence of the invention.
                                                                                                             AGCTCAAACTCACTCCTTCAGCAATTTTTGATCGGAACCGGAAGGATGAACTGCCTCGGT
                  AGCTCAAACTCACTCCTTCAGCAATTTTTGATCGGAACCGGAAGGATGAACTGCCTCGGT
                                                                  TACACCAAAAACGACTGCTGGCCTCAACTGCCTCCTCCTCCCCTGCCAGTGTTATGG
                                 TGCAACTGGAGTGGATTGATAGCATCTGCATGCCTTTGTATCAGGCACTGGTGAAGGTCA
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                                              GAGATGCTGAAGCAGGCAAGAACATTTCAGAAATGTGCTCAGTGCCACAGTGG
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        GACATTCATTTTGATGACTTTTCTCTCGACGTTGATGCCATGATCACAGGTGCTCTCCGG
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The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides the protein and coding sequences of nove human and rat type II phosphodiesterases (PDEII). These are useful for studying intracellular signal transduction mechanisms, in screening highly-selective inhibitors as drugs for treating diseases associated with the enzymes and for the identification or selection of selective inhibitory action against multiple type phosphodiesterases. The present sequence is a coding sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 AGGATCGACGATTCAATGATGAAATCGACAAGCTGACTGGATACAAGACAAAATCATTAT
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                                                                                                                    The present sequence encodes a human polypeptide which has phosphodiesterase elytypeptide and phosphodiesterase polypeptide and polynucleotide are used for the treatment and prevention of diabetes, ischemic heart disease, hypertension, nephritis, pancreatitis, ulcers, allerdys, asthma, rheumatism, osteoporosis, pain, anxiety, schizophrenia, manic depressive psychosis, parkinson's disease, dementia, infectious diseases, and malignant tumours.
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 Nakamura
                                                    Polypeptides with phosphodiesterase activity and DNA for t diabetes, ischemic heart disease, hypertension, nephritis, pancreatitis, ulcers, allergies, asthma
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                ATATCTAACGCTCAGCTCTTTGCTGCCTCAAGGAAAGAATATGAAAGAAGCAGAGCTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences of novel human and rat type 11 phosphodiesterases (PDBII). These are useful for studying intracellular signal transduction mechanisms, in screening highly-selective inhibitors as drugs for treating diseases associated with the enzymes and for the identification or selection of selective inhibitory action against multiple type phosphodiesterases. The present sequence is a coding sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.0%; Score 1684; DB 22; Length 3492; 88.5%; Pred. No. 0;
                                                                                  phosphodiesterase; PDE11; signal transduction;
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                                                       phosphodiesterase coding sequence
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                                                                                                                                                      Location/Qualifiers
241. 2298
/*tag= a
/product= "PDE11"
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2000JP-0163875.
                          (first entry)
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                                                                                               inhibition; ds
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P-PSDB; AAG62679.
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Matches 1838; Conserv
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01-JUN-2000;
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                                   CACAATATCTTTGCTAACCTGTCCTCCAAGGAATATAGTGACCTTATGCAGCTTTTGAAG
                                                                                                CAGTCAATATTGGCAACAGACCTCACGCTGTACTTTGAGGAGGAGAACTGAATTCTTTGAÄ
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169. 2976
/*tag= a
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                                                                                                                                                                                                                                                               The present invention provides the protein and coding sequences of nove-
human and rat type 11 phosphodiesterases (PDE11). These are useful for
studying intracellular signal transduction mechanisms, in screening
highly-selective inhibitors as drugs for treating diseases associated
with the enzymes and for the identification or selection of selective
inhibitory action against multiple type phosphodiesterases. The present
sequence is a coding sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1199 AGGTTCCTGAGGGTGCTCCATTTACAGAAGACGACGAAAAAGTTATGCAGATGTATCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                  Length 4170;
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             22-DEC-1999; 99JP-0364866.
01-JUN-2000; 2000JP-0163875.
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                                                       (TANA ) TANABE SEIYAKU CO.
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                                                                                      Yuasa K,
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The present sequence is that of CDNA encoding HSPDE10A1 (see AAY95521), a novel human cyclic nucleotide phosphodiesterase. The CDNA was initially identified in Incyte Clone 826776 from the prostate CDNA library PROSTHO4 using BAST3 analysis and human phosphodiesterase 5 as query. Full-length cDNA sequences of HSPDE10A1 were obtained from a human skeletal muscle library using the complete CDNA insert of Incyte Clone 826776 as probe. The invention provides expression vectors, host cells, antibodies, agonists and antagonists, as well as methods for diagnosing, treating or preventing disorders associated with expression of HSPDE10A1, especially cancer and immune disorders. A fragment of the present sequence from about nucleotide 1168 to nucleotide 1212 is useful in hybridisation or amplification technologies to
                    AGCTGCCTCGGCTGCAACTGGAGTGGATTGACAGCATCTGCATGCCTTTGTATCAGGCCT
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                                                                                                                        CTGCCAGTGTTATGGTAGCCAAGGAAGACAGGAACTAATAACTCGAGGCATGC
                                                                                                                                                                                                                                                                          nucleotide phosphodiesterase; HSPDE10A1; human; cancer; disorder; diagnosis; therapy; ss.
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                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                Sequence 2513 BP; 761 A; 528 C; 565 G; 659 T; 0 other;
                                                                                                                                                       dementia, infectious diseases, and malignant tumours
                                                                                                                                                                                                           DB 22;
                                                                                                                                                                                                                                    2;
                                                                                                                                                                                                         Score 1421.8;
Pred. No. 0;
0; Mismatches
             diabetes, ischemic heart disease, hypert
pancreatitis, ulcers, allergies, asthma
                                                   Claim 3; Page 82-86; 105pp; Japanese.
                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                          68.4%;
99.9%;
                                                                                                                                                                                                                                  Matches 1423; Conservative
                                                                                                                                                                                                                       Local Similarity
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2018

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GGAGCATCACCATTTCAACCACGCCGTGATGATCCTTCAAAGTGAGGGTCACAATATCTT 1516
                                                                                                                                                                                                                                                                                                                                  Human; phosphodiesterase; PDE-like enzyme; benign prostate hyperplasia; urinary incontinence; erectile dysfunction; cardiovascular disorder; cancer; diabetes: ischaemic disease; myocardial infarction; cytostatic; vasodilator; cardiant; gene; ss.
                                                                                                                                                                                                             1397 TGCCTTCCAAGCTAAGAGTGGCTCTGCCCTGGCCCAACTCTATGGAACCTCTGCTACCTT
                                                                  1023 GGAGCATCACCATTTCAACCACGCCGTGATGCTTCAAAGTGAGGGTCACAATATCTT
  GCTGGGGATGGTACAGAAATTTAAAATTGACTATGAGACACTGTGTAGGTGGCTTTTGAC
                           GCTGGGGATGGTACAGAAATTTAAAATTGACTATGAGACACTGTGTAGGTGGCTTTTTGAC
                                                     AGTGAGGAAAAACTATCGGATGGTTCTATACCACACAACTGGAGACATGCCTTCAACGTGTG
                                                                                                                                                            AATTTTAGCGGTGATTGTGGGATGCCTGTGTCATGACCTCGACCACGGGGAACCAACAA
                                                                                                                                                                                                                                                                                                                     TGCTAACCTGTCCTCCAAGGAATATAGTGACCTTATGCAGCTTTTGAAGCAGTCAATATT
                                                                                                         TCAGCTGATGTTCGCGATGTTAACCACTGCTGGGTTTCAAGACATTCTGACGAGGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "CDS does not include start and stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Human PDE-like protein"
                                                                                                                                                                                                                                                                                                                                                                         GGCAACAGACCTCACGCTGTACTTTGAGAGGA 1608
                                                                                                                                                                                                                                                                                                                                                                                                 1143 GGCAACAGACCTCACGCTGTACTTTGAGGAGA 1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human PDE-like enzyme encoding cDNA #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD28571 standard; cDNA; 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUN-2000; 2000US-213998P.
25-MAY-2001; 2001US-293221P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="./note=".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-JUN-2001; 2001WO-EP07289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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P-PSDB; AAD28571.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of CDNA encoding HSPDE10A2 (see
AAY95522), a novel human cyclic nucleotide phosphodiesterase. The
CDNA was initially identified in Incyte Clone 856776 from the
prostate CDNA library PROSTUTO4 using BLAST analysis and human
phosphodiesterase 5 as query. Full-length CDNA sequences of
the Complete CDNA insert of Incyte Clone 826776 as probe.
CT PRDE10A2 were obtained from a human skeletal muscle library using
the complete CDNA insert of Incyte Clone 826776 as probe.
CT The invention provides expression vectors, host cells, antibodies,
agonists and antagonists, as well as methods for diagnosing,
treating or preventing disorders associated with expression of
CT SPDE10A, sepecially cancer and immune disorders. A fragment of
the present sequence from about nucleotide 1187 to nucleotide 1227
is useful in hybridisation or amplification technologies to
distinguish HSPDE10A2 sequences from related sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human cyclic nucleotide phosphodiesterases, referred as HSPDE10A1 HSPDE10A2, useful for treating and preventing cancer and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                      557 ACCAGTGGTGAAATTTACCAAATCCTTTGAATTGATGTCCCCAAAGTGCAGTGCTGATGC
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 Harrow
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Bandman O,
                                                                                                                                                                                                                                                                                                                                                                                50.3%; Score 1045.6; DB 2.
llarity 99.6%; Pred. No. 1.1e-314;
Conservative 0; Mismatches 4;
 'n
                                                                                                                   Claim 4; Page 85-86; 96pp; English.
 Fawcett
 ٦,
 Lanfear
                        WPI; 2000-452539/39.
P-PSDB; AAY95522.
                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 1048; Conserv
Phillips SC,
                                                                                         disorders
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                                                                                               The present invention relates to human phosphodiesterase (PDE)-like enzymes and their corresponding polynuclectides. The invention also relates to reagents which regulate PDE-like enzyme activity and reagents which bind to human PDE-like enzyme gene products which can be used to regulate degradation of cGMP. Sequences of the invention are useful for modulating the activity of a PDE-like enzyme in a disease such as urinary incontinence, benign prostate hyperplasia, erectile dysfunction, cancer, diabetes or cardiovascular disorder (e.g. ischaemic diseases, myocardial infarction). The present sequence is a cDNA encoding human PDE-like
                                                                                                                                                                                                                                                                                                                                                                                                    290
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polynucleotide encoding a human phosphodiesterase-like enzyme, or treating a disease such as urinary incontinence, benign hyperplasia, erectile dysfunction, diabetes, cancer or
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                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                             Human; cGMP phosphodiesterase V; inhibitor; tricyclic compound; cyclic GMP phosphodiesterase inhibitor; erectile failure; feminine function failure; ds.
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                                                                                                                                                                                                                                                                                      DB 24; .Length 426;
                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                       Sequence 426 BP; 137 A; 76 C; 94 G; 119 T; 0 other;
                                                                                                                                                                                                                                                                                   18.7%; Score 388.8; DB 24 99.5%; Pred. No. 2.3e-110;
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                                                                        1b; Fig 4; 165pp; English.
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                                                                                                                                                                                                                                                                                                Local Similarity 99.5
les 390; Conservative
                                            cardiovascular disorder
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1153 ICAATTACATGTATGCTCAGTATGTCAAAAATACTATGGAACCACTTAATATACCCAGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes cyclic GMP (cGMP)-specific phosphodiesterase inhibitors comprising tricyclic compounds or their salts. The inhibitors are useful for the treatment and prevention of erectile failure and feminine function failure. The compounds have excellent cGMP-phosphodiesterase inhibitory action. The present sequence encodes human cGMP phosphodiesterase V, which is used in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                             Tricyclic compounds having cyclic GMP-specific phosphodiesterase inhibitory action useful as pharmaceuticals, and preparation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 356.6; DB 21;
Pred. No. 7.7e-100;
0; Mismatches 854;
                                                                                                                                                                                                                                                                                                                                                                                                          Example 117; Page 68-69; 71pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 example from the present invention.
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52.0%;
99JP-0204103
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Matches 954; Conservative
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17.2
Best Local Similarity 52.0
Matches 954; Conservative
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P-PSDB; AAY78940.
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                                    TGCAGATCAACGACTTTTTGAGGCTTTTTGTCATCTTTTGTGGACTTGGCATCAACAACAC
                                                                        AATTATGTATGATCAAGTGAAGAAGTCCTGGGCCAAGCAGTCTGTGGCTCTTGATGTGCT
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                                                                                                                       ---GAACTIGCCATGGATGACATICATITIGATGACTITITCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New phosphodiesterase V useful for screening potential phosphodiesterase inhibitors for treatment of hypertensive and allergic diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phosphodiesterase V; human; hypertension; pulmonary hypertension; atherosclerosis, cerebral infarction; allergic rhinitis; kidney fidiabetic complication; glaucoma; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human phosphodiesterase V nucleotide sequence #2.
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Pred. No. 7.7e-100;
0; Mismatches 854;
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CATGCCTTTGTATCAGGCACTGGTGAAGGTCAACGTGAAACTGAAGCCGATGCTAGATTC 1948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiarteriosclerotic; antiallergic; antianginal; cardiant; hypotensive; antiarteriosclerotic; antiallergic; antiasthmatic; nephrotropic; immunostimulant; ophthalmological; vasotropic; pyrimidine-5-carboxamide; cGMP-specific PDE inhibitor; heart disorder; allergy; immunodeficiency; eye disorder; fertility; ss.
                                                                                                                1829 TGATCGGAACCGGAAGGATGAACTGCCTCGGTTGCAACTGGAGTGGATTGATAGCATCTG
                                                                                                                                                                                                                                                                                                      GAACAGGGAGAAGAAAAACAAAAATCCCAAGTATGCAAGTTGGGTTCATAGATGCCATCTG
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                                                                                                                                                                                                                    TTCTGCAATTACAAAACCCTGGCCTATTCAACAACGGATAGCAGAACTTGTAGCAACTGA
                                                                                                                                                                                                                                           TTTCAACCACGCGTGATGATCCTTCAAAGTGAGGGTCACAAAATCTTTGCTAACCTGTC
                                 1929 TITTGACCAGTGCCTGATGATTCTTAATAGTCCAGGCAATCAGATTCTCAGTGGCCTCTC
                                                         CTCCAAGGAATATAGTGACCTTATGCAGCTTTTGAAGCAGTCAATATTGGCAACAGACCT
                                                                                                    CACGCTGTACTTTGAGAGGAGAACTGAATTCTTTGAACTTGTCAGTAAAGGAGAATACGA
                                                                                                                                                   TTGGAACATCAAAAACCATCGTGATATATTTCGATCAATGTTAATGACAGCCTGTGACCT
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                                                                                                                                                                                invention relates to novel pyrimidine-5-carboxamide compounds which may be used as cGMP-specific phosphodiesterase (CGMP-PDE) inhibitors, cGMP-PDE-1 inhibitors, cGMP-PDE-1 inhibitors are useful for treating and preventing angina pectoris, cardiac insufficiency, myocardial ischaemia, hypertension, pulmonary hypertension, arteriosclerosis, allergic disorders, asthma, nephropathies, cerebral fibrosis, immunodeficiency, eye disorders and male or female sexual dysfunction.
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                                                                                                                                                                      present sequence encodes human phosphodiesterase-V (PDE-V).
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                                                                            e cGMP-specific
e.g. angina pectoris,
                                                                                                                                                                                                                                                                                                                                                        Score 356.6; DB 22; Length
Pred. No. 7.7e-100;
0; Mismatches 854; Indels
                                                                                                                                                                                                                                                                                                                           Sequence 2499 BP; 778 A; 493 C; 563 G; 665 T; 0 other;
                                                                        New pyrimidine-5-carboxamide compounds are phosphodiesterase inhibitors for treating eallergies and immunodeficiencies
                                                                                                                                      Example 3; Page 333-334; 241pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (cGB-PDE) DNA
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Thomas MF
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Pred. No. 8e-100;
0; Mismatches 854;
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Sonnenburg WK,
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Mcallister-lucas LM, S
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                                                   TAAGAGTGGCTCTGCCCTGGCCCAACTCTATGGAACCTCTGCTACCTTGGAGCATCACCA
                     TTTCAACCACGCGGGGTGATGATCCTTCAAAGTGAGGGTCACAATATCTTTGCTAACCTGTC
                                                                         CTCCAAGGAATATAGTGACCTTATGCAGCTTTTGAAGCAGTCAATATTGGCAACAGACCT
                                                                                                        CACGCTGTACTTTGAGAGGAGAACTGAATTCTTTGAACTTGTCAGTAAAGGAGAATACGA
                                                                                                                TTGGAACATCAAAAACCATCGTGATATTTTCGATCAATGTTAATGACAGCCTGTGACCT
                                                                                                                                              TGGAGCCGTGACCAAACCGTGGGAGATCTCCAGACAGGTGGCAGAACTTGTAACCAGTGA
                                                                                                                                                                                                2366 ATTTTTGATCAAGGAGACAGAGAGAAAAGAACTCAACATAGAACCCCACTGATCTAAT
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                                                                                                                                                                                                                                            GAACAGGGAGAAAAAAAAAAAATCCCAAGTAGCAAGTTGGGTTCATAGATGCCATCTG
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93US-0068051.
95US-0463949.
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27-MAY-1993;
05-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                  cyclic guanosine monophosphate (cGMP) binding, cGMP-specific phosphodiesterase (designated cGB-PDE). The enzymes can be recombinantly expressed by standard recombinant methodogy. Antibodies specifically immunoreactive with the cGB-PDE enzyme may be used to modulate the activity of the cGB-PDE enzyme. Additionally, they may be used in assays et gry me linked immunoabsorbant assays (ELISAs) to detect the presence of the enzyme in bloopical samples. The present sequence represents a cDNA encoding the human cGB-PDE enzyme.
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                                                                                                                                                                                                                                                                                                                                                                               invention provides nucleotide sequences encoding bovine and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169 AGGATCGACGATTCAATGATGAATCGACAAGCTGACTGGATACAAGACAAAATCATTAT
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                                                                             Kadlecek A;
Thomas MK;
                                                                                                                                                                                                                                         specific for {\tt CGMP-binding} , {\tt CGMP-specific} sterase useful for detecting and modulating the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2645 BP; 813 A; 537 C; 609 G; 686 T; 0 other;
                                                                             f, Francis SH,
Sonnenburg WK,
                                                                                                                                                                                                                                                                                                                       Example 6; Columns 49-56; 42pp; English.
                                                                             Corbin JD, Ferguson KM, McAllister-lucas LM, S
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52.0%;
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Best Local Similarity 52.0
Matches 954; Conservative
                                                                                                                                                                                                                                                                     phosphodiesterase useful
(UYVA-) UNIV VANDERBILT (UNIW ) UNIV WASHINGTON
                                                                                                                                                         WPI; 1999-539597/45.
                                                                                                                                                                                       P-PSDB; AAY14991
                                                                                                      Loughney K,
                                                                                                                                                                                                                                            Antibodies
                                                                                Beavo JA,
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Op	Qy Db	Οy	qq	Qy Dp	٥y	Op	Qy Dp	Qy	Oy Db	Oy Db	٥٧ وې	g & g	. 40 00	Qy	Qy	Qy Db	Qy	Qy	Qy Db	Qy . Db

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1889	2486	1949	2546
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Matches 1505; Conservative
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-464-410A-22
US-08-464-410A-22
US-08-464-410A-12
US-08-250-8478-12
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ALIGNMENTS

CAGCATTGCTGAGCTGGTTGCTTCAACAGGCCTTCCAGTGAACATCAGTGATGCCTACCA 557 ACCAGTGGAAATTTACCAAATCCTTTGAATTGATGTCCCCAAAGTGCAGTGCTGATGC GGATCCGCGCTTTGATGCAGAGGCAGACCAGATATCTGGTTTTCACATAAGATCTGTTCT TTGTGTCCCTATTTGGAATAGCAACCACCAAATAATTGGAGTGGCTCAAGTGTTAAACAG ACTTGATGGGAAACCTTTTGATGATGCAGATCAACGACTTTTTGAGGCTTTTGTCATCTT Gaps Length 1784; . 0 Indels DB 3; Sequence 2. Application US/09226741
Patent No. 6100037
GENERAL INFORMATION:
APPLICANT: Phillips, Stephen C.
APPLICANT: Pandman, Olga
TITLE OF INVENTION: HUMAN CYCLIC NUCLEOTIDE PDES
FILE REFERENCE: PF-0623 US
CURRENT APPLICATION NUMBER: US/09/226,741
CURRENT APPLICATION NUMBER: US/09/226,741
CURRENT APPLICATION NUMBER: US/09/226,741
SOURBER OF SEQ ID NOS: 7
SEQ TURE OF SEQ ID NOS: 7 Score 1503.8; Mismatches Pred. No. 0; . () 72.48; ; OTHER INFORMATION: HSPDE10A1 US-09-226-741-2

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QY 1997 GCTGGCCTCAACTGCCTCATCCTCCTGCCAGGTAGGTAGCCAAGGAAGACAG 2056 DD 1157 GCTGGCCTCAACTGCCTCCTCCCTGCCAGTTATGGTAGCCAAGGAAGACAG 1616 QY 2057 GAACTAA 2063 DD 1617 GAACTAA 1623	RESULT 2 US-09-595-514-2 US-09-595-514-2 ; Patent No. 6416991 ; GENERAL INFORMATION: ; APPLICANT: Phillips, Stephen C. ; APPLICANT: Fawcett, Lindaay ; APPLICANT: Bandman, Olas	TITLE OF INVENTION: HUMBER CYCLIC NUCLEOTIDE PDES FILE REFERENCE: PF-0623-1 CIP CURRENT APPLICATION NUMBER: 02/09/595,514 CURRENT FILING DATE: 2000-06-41 PRIOR APPLICATION NUMBER: 09/226,741 PRIOR FILING DATE: 1999-01-07 NUMBER OF SEQ ID NOS: 7 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 2 LEWGTH: 1784	; TYPE: DNA ; ORGANISM: HOMO SAPIENS ; OTHER INFORMATION: HSPDE10A1 US-09-595-514-2 Query Match 72.4%; Score 1503.8; DB 4; Length 1784; Best Local Similarity 99.9%; Pred. No. 0; Matches 1505; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	Qy 557 ACCAGTGGTGAAATTTACCAAATCCTTTGAATTGATGTGCCCCAAAGTGCAGTGCTGATGC 616 117 ACAGTGGTGAAATTTACCAAATCCTTTGAATTGATGTCCCCAAAGTGCAGTGCTGATGC 776 Qy 617 TGAGAACAGTTCAAAGAAACCATGGAGAAATCATACATCATACTCCGACTGCTAAAAAAAA	677 CAGCATTGCTGACTGCTTCAACAGGCCTTCCAGTGAACATCAGTGATGCTACCA 677 CAGCATTGCTGACTGCTTCAACAGGCCTTCCAGTGAACATCAGTGATGCCTACCA 737 GCATTGCTGAGTGCTTCAACAGGCCTTCCAGTGAACATCAGTGATGCTTACCA 737 GCATCCGCCTTTGATGCAGAGCAGACCAGATATCTGGTTTTCAACAAAGATCTGTTCT 1111111111111111111111111111111	Oy 797 TTGTGTCCCTATTTGGAATAGCAACCACCAATAATTGGAGTGGCTCAAGTGTTAAACAG 856	TTGTGGACTTGGCATCAACAACAATTATGTATGATCAAGTGAAGAAGTCCTGGGCCAA 97 TTGTGGACTTGGCATCAACAACAATTATGTATGATCAAGTGAAGAAGTCCTGGGCCAA 97 TTGTGGACTTGGCATCAACAACAATTATGTATGATGATGAAGAAGTCCTGGGCCAA 93 GCAGTCTGTGGCTGTTGATGTGTATCATACCATGCAACATTCAAAAGCTGAAGTTGA 10	1037 CAAGTTTAAGGCAGCCAACATCCTTGGTGCAGAACTTGCCATCATGATTT 10 11037 CAAGTTTAAGGCAGCCAACATCCTTGGTGTCAGAACTTGCCATCATGATTT 15 597 CAAGTTTAAGGCAGCCAACATCCCTCTGGTGTCAGAACTTGCCATCATTTT 15
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APPLICANT: Laffear, Jerry
APPLICANT: Fawcett, Lindsay
APPLICANT: Fawcett, Lindsay
TITLE OF INVENTION: HUMAN CYCLIC NUCLEOTT
FILE REPERENCE: PF-0623 US
CURRENT APPLICATION NUMBER: US/09/226,743;
CURRENT PILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0;
SEQ ID NO 4 Query Match 50.3%; Best Local Similarity 99.6%; Matches 1048; Conservative ; OTHER INFORMATION: HSPDE10A2 US-09-226-741-4 SAPIENS ORGANISM: HOMO LENGTH: 1982 783 1277 qq δ

Sequence 4, Application US/09226741 Patent No. 6100037

US-09-226-741-4

Page 4

Db 423 ACTTGATGGGAAACCTTTTGATGATGCAGGATCAACGACTTTTTGAGGCTTTTGTCATCTT 4 Qy 917 TTGTGGACTTGGCATCAACAACAACAACAATTATGTATGAAGAAGTGAAGAAGTCCTGGGCCAA 9	Db	1037 CAAGITTAAGGCAGCCAACATCCCTCTGGTGTCAGAACTTGCCATCGATGACATTCATT	QY 1097 TGATGACTTTTCTCTCGACGTTGATGCCATGATCACAGCTGCTCTCCGGATGTTCATGGA 115 Db 663 TGATGACTTTTCTCTCGACGTTGATGCCATGATCACAGCTGCTCTCCGGATGTTCATGGA 722	Oy 1157 GCTGGGGATGGTACAGAAATTTAAAAȚTGACTATGAGACACTGTGTAGGGGGCTTTTGAC 121 Db 723 GCTGGGGATGGTACAGAAATTTAAAATTGACTATGAGACACTGTGTAGGTGGCTTTTGAC 782	Oy 1217 AGTGAGGAAAAACTATCGGATGCTTCTATACCACAACTGGAGACATGCCTTCAACGTGT 127 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	1337 AATTTAGGGGGGGATGTTGTGGGGGGGGGGGGGGGGGG	DB 903 AATTTTAGCGGTGATTGTGGGATGCCTGTGTCATGACCACACACA	OY 1457 GGAGCATCACCATTTCAACCACGCGTGATGATCCTTCAAAGTGAGGGTCACAATATCTT 151	QY 1517 TGCTAACCTGTCCAAGGAATATAGTGACCTTATGCAGCTTTTGAAGCAGTCAATATT 157 11 11 11 11 11 11 11	Qy 1577 GGCAACAGACCTCACGCTGTACTTTGAGAGGA 1608 	RESULT 5 US-08-480-547A-22 Sequence 22, Application US/08480547A Patent No. 5652131 GENERAL INFORMATION: APPLICANT: Beavo, Joseph A. APPLICANT: Corbin, Jackie D. APPLICANT: Perguson, Kenneth M.	la M.	rase Materials and Metherstein, Murray & Borun	o. wacker Di
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1291 TCAGTAAGGATAAAAGATTTCCCTGGACAACTGAAAATACAGGAAATGTAAACCAGCAGT 1350
                                                              1351 GCATTAGAAGTTTGCTTTGTACACCTATAAAAAATGGAAAGAAGAATAAAGTTATAGGGG 1410
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                                 AGACCAGATATCTGGTTTTCACATAAGATCTGTTTTGTGTCCCTATTTGGAATAGCAA
                                                                                                                                                                                                                                                                                    ATCATACCATGCAACATGTTCAAAAGCTGAAGTTGACAAGTTTAAGGCAGCCAACATCCC
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                                                                                           821 CCACCAAATAATTGGAGTGGCTCAAGTGTTAAACAGACTTGATGGGAAACCTTTTGATGA
                                                                                                                                                          881 TGCAGATCAACGACTTTTTGAGGCTTTTGTCATCTTTTGTGGACTTGGCATCAACAACAC
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                                                   COMPOURE: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,547A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5652131and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 356.6; DB 1;
Pred. No. 1.6e-105;
0; Mismatches 854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 32791
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEPAX: (312) 474-6448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.2%;
52.0%;
                                            Floppy disk
                                                                                                                                                                                                                                                                                                                              LENGTH: 2645 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Matches 954; Conservative
                            COMPUTER READABLE FORM:
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US-08-480-547A-22
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                                            MEDIUM TYPE:
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OY 169 AGGATCGACGATTCAATGATGAAATCGACAAGCTGACTGGATACAAGACAAAATCATTAT 228	QY 229 TGTGCATGCCTATCGGAGGAGTGATGATATATGGTGTGGGCCCAAGCGATAAATA 288	OY 289 AGATTCCTGAAGGAGCTCCATTTACTGAAGATGAAAAAGTTATGCAGATGTATC 345	OY 346 TICCATITIGIGGAATCGCCATATCIAACGCTCAGCTCTTIGCTGCCTCAAGGAAAGAAT 405	OY 406 ATGAAAGAAGCAGAGCTTTGCTAGAGGTGGTTAATGACCTCTTTGAAGAACAGACTGACC 465	Qy 466 TGGAGAAAATTGTCAAGAAAATAATGCATCGGGCCCAÁACTCTGCTGAAATGTGAGGGT 525	OY 526 GTTCTGTTTACTCCTAGAGGACATCGAATCACCAGTGGTGAAATTTACCAAATCCTTG 585	Oy 586 AATTGATGTCCCCAAAGTGCAGTGCTGAGAACAGTTTCAAAGAAACCATGGAGA 645	646 AATCATCTCGACTGCCTAATAAATAACGCATTGCTGAGCTTGCTT	706 GCCTTCCAGTGAACATCAGTGATGCCTACCAGGATCCGCGCTTTGATGCAGGGC	OY 761 AGACCAGATATCTGGTTTTCACATAAGATCTGTTCTTTGTGTCCCTATTTGGAATAGCAA 820	OY 821 CCACCAAATAATIGGAGTGGCTCAAGTGTTAAACAGACTTGATGGAAACCTTTGATGA 880		QY 941 AATTATGTATGATCAAGTGAAGATCCTGGGCCAAGCAGTCTGTGGCTCTTGATGTGT 1000	OY 1001 ATCATACCATGCAACATGTTCAAAAGCTGAAGTTGACAAGTTTAAGGCAGCCAACATCCC 1060	Qy 1061 TCTGGTGTCAGAACTTGCCATGACATTCATTTGATGACTTTTCTCT 1111	OY 1112 CGACGTTGATGCCATGATCACAGCTGCTCTCCGGATGTTCATGGAGCTGGGGATGGTACA 1171	OY 1172 GAAATTTAAAATTGACTATGACACACTGTAGGTGGCTTTTGACAGTGAGGAAAACTA 1231
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AGCATCTG 1888 GCCATCTG 2485	TGCTAGATTC 1948 GCTAGATGG 2545																. Gaps 6;
ACTGGAGTGGATTGAT. 	GAAACTGAAGCCGATGG 	1981 2578			·		ic GMP-Specific als and Methods	Murray & Borun Drive		1.25				٠.			1; Length 2645; 05; Indels 25;
TGATCGGAACCGGAAGGATGAACTGCCTCGCTTGCAACTGGAGTGGATTGATAGCATCTG 1 1 1 1 1 1 1 1 1	CATGCCTTTGTATCAGGCACTGGAAGGTCAACGTGAAACTGAAGCCGATGCTAGATTC	949 AGTAGCTACAAACAGAAGTAAGTGGGAAGAGCT 19 	R250847B	A	b. eth M on H.	as, Linda M. lliam K. a K.	Cyclic GMP-Binding, Cyclic GMP-Specific Phosphodiesterase Materials and Methods 23 SS:	Gerstein, S. Wacker	, 	compatible PC-DoS/MS-DoS I Release #1.0, Version #1 ATA:	US/U8/25U, 84/B	US 08/068,051 11993 FION: 1, Greta E.	32083 32083 ION: 00	22:			; Score 356.6; DB 1; ; Pred. No. 1.6e-105; 0; Mismatches 854;
GATCGGAACCGGAAGG 	ATGCCTTTGTATCAGGC/ 	GTAGCTACAAACAGAA TGCAGAAGAACAGGC	22 Application HS/0	5702936 NFORMATION: NT: Beavo, Joseph A.		McAlliste Sonnenbur Thomas, h	畄	E	00 04 14 15 16 16 16 16 16 16 16 16 16 16 16 16 16	SYSTEM: PC SYSTEM: PC Patentin F LICATION DAT	10 4	APPLICATION WUBBER: US 08/068 FILING DATE: 27-MAY-1993 ATTORNEY/AGENT INFORMATION: NO. 5702936and, Greta E DEFICEMENT ON MINURED C. 202	REFERENCE/DOCKET NUMBER: 35,002 REFERENCE/DOCKET NUMBER: 32 TELECOMMUNICATION INFORMATION: TELEPHONE: (312) 474-6300 HEFFERY. (312) 474-6300	(512) 4/4 0446 25-3856 FOR SEQ ID NO: 14RACTERISTICS:	nucleic acid nucleic single SDNESS: single SY: linear	: CDS: 122636	17.2%; Similarity 52.0%; 4; Conservative
Qy 1829 T Db 2426 G	Oy 1889 C 1 Db 2486 C	Qy 1949 A Db 2546 C	RESULT 6 US-08-250-847B-22 : Sequence 22, An	GENERAL INFORMATION: APPLICANT: Beavo,	APPLICANT: APPLICANT: APPLICANT: APPLICANT:	APPLICANT: APPLICANT: APPLICANT: APPLICANT:	TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES; CORRESPONDENCE ADDR	; ADDRESSEE: ; STREET: 6: ; CITY: Chic; ; STATE: Il.	COUNTRY: ZIP: 60 COMPUTER RI MEDIUM T	COMPOTER: COMPOTER: COETWARE: CURRENT APPI	FILING DATE: CLASSIFICATION: PRIOR APPLICATION:	APPLICAT FILING D ATTORNEY/A NAME: N PECTEURY	REFERENCE/I REFERENCE/I TELEPHONE: TELEPHONE:	INFORMATION SEQUENCE CI	TYPE: nucleic STRANDEDNESS: TOPOLOGY: lin	MOLECOLE 11F 	Query Match Best Local Sir Matches 954;

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751 AGGATCCTCGGTTCAATGCAGAAGTTGACCAAATTACAGGCTACAAGACACAAAGCATTC 810
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                                                                                                                            OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Pred. No. 1.6e-105;
                                                                                                                                                                                    APPLICATION NUMBER: US/08/463,949A
                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/068,051
FILING DATE: 27-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                               NAME: No. 595583and, Greta E. REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32706
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TELESTAX: (312) 474-0448
TELEX: 25-3856
INPORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 2645 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                            Eloppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
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52.0%;
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                                                     ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: 12..2636
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 Chicago
Illinois
Y: USA
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                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-463-949A-22
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Best Local Simi
Matches 954;
                                    COUNTRY:
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APPLICANT: Ferguson, Kenneth M.
APPLICANT: Francis, Sharron H.
APPLICANT: Kadlecek, Ann
APPLICANT: Loughney, Kate
APPLICANT: McAllister-Lucas, Linda M.
APPLICANT: Sonnenburg, William K.
APPLICANT: Thomas, Melissa K.
TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
TITLE OF INVENTION: Phosphodiesterase Materials and Methods
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S. Wacker Drive
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ADDRESSEE: Marshall,
STREET: 6300 Sears To
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                                                                                                                                                                                                                                        1949 AGTAGCTACAAACAGAAGTAAGTGGGAAGAGCT 1981
                                                                                                                                                                                                                                                                        2546 CTGCAGAAGAACAGGCAGAAATGGCAGGCCCT 2578
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ATTORNEY/AGENT INFORMATION:
NAME: NO. 6037119and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32705
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ferguson, Kenneth M.
APPLICANT: Francis, Sharron H.
APPLICANT: Kadlecek, Ann
APPLICANT: Loughney, Kate
APPLICANT: McAllister Lucas, Linda M.
APPLICANT: Sonnenburg, William K.
APPLICANT: Thomas, Mellissa K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/464,410A FILING DATE: June 5, 1995
                                                                                                                                                                                                                                                                                                                                                           Sequence 22, Application US/08464410A Patent No. 6037119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
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IBM PC compatible
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                              Beavo, Joseph A.
Corbin, Jackie D.
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LENGTH: 2645 base pairs
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CORRESPONDENCE ADDRESS:
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Illinois
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GENERAL INFORMATION:
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APPLICANT:
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Length 2645; DB 3; Score 356.6; 17.28;

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ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Illinois
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                             AGGATCGACGATTCAATGATGAAATCGACAAGCTGACTGGATACAAGACAAAATCATTAT
                                         TGTGCATGCCTATCCGAAGCAGTGATGGTGAGTTATTGGTGGCCCCAAGCGATAAATA
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  ed. No. 1.6e-105;
Mismatches 854;
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 52.0%;
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2545 TGATCGGAACCGGAAGGATGAACTGCCTCGGTTGCAACTGGAGTGGATTGATAGCATCTG 1888 CATGCCTTTGTATCAGGCACTGGTGAAGGTCAACGTGAAACTGAAGCCGATGCTAGATTC 1948 GAACTTCCAGATGAAACATGAGGTTCTTTGCAGATGGATTTTAAGTGTTAAGAAGAATTA 1828 CACGCTGTACTTTGAGAGGAGAACTGAATTCTTTGAACTTGTCAGTAAAGGAGAATACGA GAACAGGGGAGAAGAAAACAAAATCCCAAGTATGCAAGTTGGGTTCATAGATGCCATCTG GATTGTGGGATGCCTGTGTCATGACCTCGACCACAGGGGAACCAACAATGCCTTCCAAGC TAAGAGTGGCTCTGCCCTGGCCCAACTCTATGGAACCTCTGCTACCTTGGAGCATCACCA TTTGGAAGATCCTCATCAAAAGGAGTTGTTTTTGGCAATGCTGATGACAGCTTGTGATCT 1289 CGCGATGTTAACCACTGCTGGGTTTCAAGACATTCTGACCGAGGTGGAAATTTTAGCGGT TITCAACCACGCCGTGATGATCCTTCAAAGTGAGGGTCACAATATCTTTGCTAACCTGTC CTCCAAGGAATATAGTGACCTTATGCAGCTTTTGAAGCAGTCAATATTGGCAACAGACCT TTGGAACATCAAAAACCATCGTGATATATTTCGATCAATGTTAATGACAGCCTGTGACCT TGGAGCCGTGACCAAACCGTGGGAGATCTCCAGACAGGTGGCAGAACTTGTAACCAGTGA TCGGATG - - - GTTCTATACCACAACTGGAGACATGCCTTCAACGTGTGTCAGCTGATGTT Sequence 22, Application PC/TUS9406066
GENERAL INFORMATION:
APPLICANT: The Board of Regents of the University of Washington TTLLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific TTLLE OF INVENTION: Phosphodiesterase Materials and Methods NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS: 1949 AGTAGCTACAAACAGAAGTAAGTGGGAAGAGCT 1981 CTGCAGAAAGAACAGGCAGAAATGGCAGGCCCT Gerstein, S. Wacker ADDRESSEE: Marshall, O'Toole, ADDRESSEE: Borun 6300 Sears Tower, 233

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1709 GTCTGATCTGGAAACAGCACTGTGTACAATTCGGATGTTTACTGACCTCAACCTTGTGCA 1768
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                                        AGACCAGATATCTGGTTTTCACATAAGATCTGTTCTTTGTGTCCCTATTTGGAATAGCAA
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                                                   PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.2%; Score 356.6; DB 5;
larity 52.0%; Pred. No. 1.6e-105;
Conservative 0; Mismatches 854;
CURPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PAtentin Release #1.0, V, CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US94/N6AFFILLER OF ARCTOR OF THE OFFILE OFFILE OFFILE OFFILE OFFILE OFFI
                                                                                   PCT/US94/06066
                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/068,051
FILING DATE: 27-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
                                                                                                                                                                                                       35,302
                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPA: (312) 474-6300
TELEFA: (312) 474-0448
TELES: 25-3856
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                       NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                        LENGTH: 2645 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Db 292 TTTGTATGCCAATTAAGAATCATAGGGAAGAGGTTGTTGGTGTAGCCCAGGCCATCAACA 351 Qy 289 AGATTCTGAAGGAGCTCCATTACTGAAGATGAAAAAGTTATGCAGATGTATG	466 TGGGGAAATTGTCAAGAAATAATGCATCGGGCCCAAACTTGCTGAAATGTCAGGAAAT	0y 821 CCACCAAATAATTGGAGTGGCTCAAGTGTTAAACAGACTTGATGGAAACCTTTTGATGA 880 1 </th <th> Db 1130 TGTGGTGCCACTGCCCAGACCTTAAAATTACTGTGCTTCAGTGCTTTTTTTT</th>	Db 1130 TGTGGTGCCACTGCCCAGACCTTAAAATTACTGTGCTTCAGTGCTTTTTTTT
Oy 1829 TGATCGGAACCGGAAGGATGAACTGCTCGGTTGCAACTGGAGTGGATTGATACCATCTG 1888 1 <td< td=""><td>RESULT 10 12-08-408-12. Application US/08480547A 15-08-12. APPLICANT: Reducek, Ann 15-08-12. APPLICANT: Francis, Sharron H. 16-08-12. APPLICANT: McAllister-Lucas, Linda M. 17-12. APPLICANT: Thomas, Melissa K. 17-12. Thomas, Melissa K. 17-12. Thomas, Melissa R. 17-12. Thomas, Melissa R. 17-12. APPLICANT: Arienathall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive 17-17. Collicago 17-18. Collicago 18-18. Colli</td><td>MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: Patentin R-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/480,547A FILING DATE: CLASSIFTCATION: 435 ATTORNEY/AGENT INFORMATION: NAME: NO. 5652131and, Greta E. REGISTRATION NUMBER: 35.302 REFERENCE/DOCKET NUMBER: 35.302 TELEPHONE: (312) 474-6300 TELEFAX: (312) 474-6300 TELEFAX: 25-3856 INFORMATION FOR SEQ ID NO: 12: SEGUENCE CHARACTERISTICS:</td><td> SENGENCE CONTRACTORS: TYPE: nucleic acid TYPE: nucleic acid</td></td<>	RESULT 10 12-08-408-12. Application US/08480547A 15-08-12. APPLICANT: Reducek, Ann 15-08-12. APPLICANT: Francis, Sharron H. 16-08-12. APPLICANT: McAllister-Lucas, Linda M. 17-12. APPLICANT: Thomas, Melissa K. 17-12. Thomas, Melissa K. 17-12. Thomas, Melissa R. 17-12. Thomas, Melissa R. 17-12. APPLICANT: Arienathall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive 17-17. Collicago 17-18. Collicago 18-18. Colli	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: Patentin R-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/480,547A FILING DATE: CLASSIFTCATION: 435 ATTORNEY/AGENT INFORMATION: NAME: NO. 5652131and, Greta E. REGISTRATION NUMBER: 35.302 REFERENCE/DOCKET NUMBER: 35.302 TELEPHONE: (312) 474-6300 TELEFAX: (312) 474-6300 TELEFAX: 25-3856 INFORMATION FOR SEQ ID NO: 12: SEGUENCE CHARACTERISTICS:	SENGENCE CONTRACTORS: TYPE: nucleic acid TYPE: nucleic acid

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AGATTCCTG---AAGGAGCTCCATTTACTGAAGATGATGAAAAAGTTATGCAGATGTATC 345
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Pred. No. 6.8e-102;
); Mismatches 813;
                                     APPLICATION NUMBER: US 08/068,051
FILING DATE: 27-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                           NAME: NO. 5702936and, Greta E. REGISTRATION NUMBER: 35,302 . REFERENCE/DOCKET NUMBER: 32083
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                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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52.3%;
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TYPE: nucleic acid
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Best Local Similarity 52.3
Matches 918; Conservative
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                             TTCTGCAATTACAAAACCCTGGCCTATTCAACAACGGATAGCAGAACTTGTAGCAACTGA
                                                                                                 1469 ITTCAACCACGCCGTGATGATCCTTCAAAGTGAGGGTCACAATATCTTTGCTAACCTGTC
                                                                         1409 TAAGAGTGGCTCTGCCCTGGCCCAACTCTATGGAACCTCTGCTACCTTGGAGCATCACCA
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APPLICANT: Thomas, Melissa K.
TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GWP-Specific
TITLE OF INVENTION: Phosphodiesterase Materials and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Marshall, O'Toole, Gerstein, 00 Sears Tower, 233 S. Wacker
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Corbin, Jackie D.
Fergusson, Kenneth M.
Francis, Sharron H.
Kadlecek, Ann
Loughney, Kate
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Chicago
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MEDIUM TYPE: Floppy disk
COMPUTER: LIBM PC compatible
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CORRESPONDENCE ADDRESS:
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US-08-463-949A-12
             US-08-463-949A-12
                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
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                                                                      APPLICANT:
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APPLICANT:
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APPLICANT:
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                                            ; Patent No.
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                                                      941 AATTATGTATGATCAAGTGAAGAGTCCTGGGCCAAGCAGTCTGTGGCTCTTGATGTGCT
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                                                                                   Ferguson, Kenneth M.
Francis, Sharron H.
Kradlecek, Ann
Loughney, Kate
McAllister-Lucas, Linda M.
Sonnenburg, William K.
Thomas, Melissa K.
VENTION: Cyclic GMP-Specific
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Drive
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Pred. No. 6.8e-102;
0; Mismatches 813;
                                                                                                                                                                                                                                                                                            Gerstein, I
S. Wacker I
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APPLICATION NUMBER: US/08/463,949A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/068,051
                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 12, Application US/08463949A
Patent No. 5955583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5955583and, Greta E.
ON NUMBER: 35,302
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6300 Sears Tower, 233
                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
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52.3%;
                                                                        Corbin, Jackie D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (312) 474-6300
                                                     Beavo, Joseph A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 27-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
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25-3856
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Best Local Similarity 52.3
Matches 918; Conservative
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IDNESS: single
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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                                    GENERAL INFORMATION:
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CLASSIFICATION:
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             TAGAAGTAATTTTGAAGAAAATAGCTGCCACTATTATCTTTTCATGCAAGTGCAGAAAT
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1667 AGCACTGTACATTAAGAGGCGAGGAGAATTTTTGAACTTATAAGAAAAAATCAATTCAA 1726
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                                1787 TTCTGCAATTACAAAACCCTGGCCTATTCAACAACGGATAGCAGAACTTGTAGCAAACTGA
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1469 TITCAACCACGCGTGATGATCCTTCAAAGTGAGGGTCACAATATCTTTGCTAACCTGTC
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                                                                                                       CTCCAAGGAATATAGTGACCTTATGCAGCTTTTGAAGCAGTCAATATTGGCAACAGACCT
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APPLICANT: McAllister-Lucas, Linda M.
APPLICANT: Sonnenburg, William K.
APPLICANT: Thomas, Malissa K.
TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific TITLE OF INVENTION: Phosphodiesterase Materials and Methods
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S. Wacker Drive
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REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32705
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
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APPLICATION NUMBER: US/08/464,410A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 12, Application US/08464410A
; Patent No. 6037119
; GENERAL INFORMATION:
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STREET: 6300 Sears Tower, 233
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APPLICANT: Francis, Sharron H.
APPLICANT: Kadlecek, Ann
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APPLICANT: Corbin, Jackie D
APPLICANT: Ferguson, Kennet
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                                                                                                                                 Gaps
                                                                                                                                 25;
                                                                                                           Length 1982;
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                                                                                                          Score 345.2; DB 3;
Pred. No. 6.8e-102;
0; Mismatches 813;
          12:
                                                                                                           16.6%;
52.3%;
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 13
SEQUENCE CHARACTERISTICS:
LENGTH: 1982 base pairs
                                                                                                                    Best Local Similarity 52.3
Matches 918; Conservative
                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                             TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                    US-08-464-410A-12
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                            TGTGGTGCCATCTGCCCAGACCCTTAAATTACTGACTTTAGCTTCAGTGACTTTGAGCT
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GENERAL INFORMATION:
APPLICANT: The Board of Regents of the University of Washing
TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
TITLE OF INVENTION: Phosphodiesterase Materials and Methods
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
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PCT-US94-06066-12
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                                                                                                        SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 16.6%; Score 345.2; DB 5; Best Local Similarity 52.3%; Pred. No. 6.8e-102; Matches 918; Conservative 0; Mismatches 813;
  Drive
 S. Wacker
                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/068,051
FILING DATE: 27-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: NOLANG, GREEA E.
RECISTRATION NUMBER: 32083
TELECOMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELERAX: 25-3856
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1982 base pairs

LENGTH: 1982 base pairs
                                                                                                                                                PCT/US94/06066
Tower, 233
                                                        LALT: COCCOUNTER FORM:
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALLIDIE
                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT
                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
6300 Sears
                                                                                           COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA
            Chicago
Illinois
                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                           FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                      USA
                                                   90909
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                                                                                                                     SOFTWARE:
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950 AAATGACGAACAGTTTCTGGAAGCTTTTGTCATCTTTTGTGGCGTTGGGGATCCAGAACAC 1009
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                                                                                                        761 AGACCAGATATCTGGTTTTCACATAAGATCTGTTCTTTGTGTCCCTATTTGGAATAGCAA
                                                                                                                                                          832 GCATTAGAAGTTTGCTTTGTACACCTATAAAAATGGAAAGAAGAATAAAGTTATAGGGG
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                                                                                                                                                                                                                  CCACCAAATAATTGGAGTGGCTCAAGTGTTAAACAGACTTGATGGGAAACCTTTTGATGA
                                                                                                                                                                                                                                                                     892 TTTGCCAACTTGTTAATAAGATGGAGGAGAATACTGGC--AAGGTTAAGCCTTTCAACCG
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1347 GTCAGTAAGGACAAAAGATTTCCCTGGACAAATGAAAACATGGGAAATATAAAACCAGCAG 1406
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                                                                                     AGATICCTG----AAGGAGCTCCATTTACTGAAGATGATGAAAAAGTTATGCAGATGTATC 345
                                                                                                                    AGAAATCAGGAAATGGTGGGACATTCACTGAAAAAGACGAAAAGGACTTTGCTGCTTACT 987
                                                                                                                                                         ITCCATTTTGTGGAATCGCCATATCTAACGCTCAGCTCTTTGCTGCTCCTCAAGGAAGAAT 405
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                                    TGTGCATGCCTATCCGAAGCAGTGATGGTGAGATTATTGGTGTGGCCCAAGCGATAAATA
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                                                                                                                                                                                                                                                                                                                              APPLICANT: Corbin, Jacken D.
APPLICANT: Ferguson, Kenneth M.
APPLICANT: Francis, Sharron H.
APPLICANT: Francis, Sharron H.
APPLICANT: Addlecek, Ann
APPLICANT: Loughney, Kate
APPLICANT: Sonnenburg, William K.
APPLICANT: Thomas, Malissa K.
TITLE OF INVENTION: Cyclic GMP-Specific
TITLE OF INVENTION: Phosphodiesterase Materials and Methods
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Pred. No. 3.9e-101;
0; Mismatches 854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/480,547A FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gerstein,
S. Wacker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: NO. 5652131and, Greta E. REGISTRATION NUMBER: 35,302
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6408
                                                                                                                                                                                                                                                             Sequence 9, Application US/08480547A Patent No. 5652131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Marshall, O'Toole, 6300 Sears Tower, 233
                                                                                                                                                                         1967 CTTGCAACTGTATGAG 1982
                                                                                                                                        CATGCCTTTGTATCAG 1904
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52.0%;
                                                                                                                                                                                                                                                                                                                       Beavo, Joseph A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 4474 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELERAX: (312) 474-0446
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 52.0
Matches 953; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Beavo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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US-08-480-547A-9
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                                                                                                                                                                                                                                                US-08-480-547A-9
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Qy Db	1288	TCGCGATGTTAACCACTGCGTTTCAAGACATTCTGACCGAGGTGGAAATTTTAGCGG	1347 2004
Qy	1348	TGATTGTGGGATGCCTGTGTCATGACCTCGACCACGGGGAACCACAATGCCTTCCAAG	1407 2064
Oy Db	1408	CTAAGAGTGGCTCTGCCCTGGCCCAACTCTATGGAACCTCTGCTACCTTGGAGCATCACCT	1467 2121
Qy Db	1468	ATTICAACCACGCCGTGATGATCCTICAAAGTGAGGTCAÇAATATCTITGCTAACCTGT 	1527 2181
Qy	.1528	1528 CCTCCAAGGAATATAGTGACCTTATGCAGCTTTTGAAGCAGTCAATATTGGCAACAGCC 1	1587 2241
Oy Db	1588	TCACGCTGTACTTTGAGAGGAGAACTGAATTCTTTGAACTTGTCAGTAAAGGAGAATACG 	1647
Qy	1648	ATTGGAACATCAAAAACCATCGTGATATATTTCGATCAATGTTAATGACAGCCTGTGACC	1707 2361
Qy Db	1708	TIGGAGCCGIGACCAAACCGIGGGAGATCICCAGACAGGGCAGAACTIGIAACCAGIG 	1767 2421
Qy Db	1768	AGTICTICGAACAAGGAGATCGGGAGATIAGAGCTCAACCACCCTCAGCAAITT 1	1827 2481
Qy Db	1828	TTGATCGGAACGGAAGGATGACTGCCTGGTTGCAACTGGAGTGGATTGATAGCATCT 1	1887 2541
Qy Db	1888	GCATGCCTTTGTATCAGGCACTGGTGAAGGTCAACGTGAAACTGAAGCCGATGCTAGATT	1947 2601
Qy	1948	1948 CAGTAGCTACAAACAGAAGTAAGTGGGAAGAGCT 1981 	

Search completed: June 20, 2003, 19:22:57 Job time : 117 secs

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Sequence 6, Appli
Sequence 7, Appli
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Sequence 9, Appli
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Sequence 11, Appl
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Sequence 12, Appl
Sequence 9, Appli
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Sequence 4, Appli
                                                                                                                (without alignments)
9411.462 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 42,
Sequence 38,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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7: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-891-216-6

US-09-891-216-7

US-10-094-168B-2

US-10-094-168B-4

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US-09-321-801-3
US-09-420-190-2
US-09-883-825-42
US-09-883-825-42
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                                                                                               June 20, 2003, 18:30:48
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Gapop 10.0 , Gapext 1.0
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              Sequence 8, Application US/09891216
Patent No. US20020103120A1
GENERAL INFORMATION:
APPLICANT RAMARISHNAN, Shyam
TITLE OF INVEWION: Regulation of Human
TITLE OF INVEWION: Regulation of Human
TITLE REFERENCE: 02973.00511
CURRENT APPLICATION NUMBER: US/09/891,216
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/233,98
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: PCT/EP01/07289
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-06-26
PRIOR FILING DATE: 2001-06-26
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-26
SPRIOR FILING DATE: 2001-05-26
SPRIOR FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 20
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100.0%; Pred. No. 0;
tive 0; Mismatches 0;
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OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 100.0
Matches 2058; Conservative
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Sequence 44, Appl

Sequence 17,

US-10-115-515-17 US-09-883-825-44

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6 GARANGCACCAGGATTTATACTAGACAAAACAAAAACAAAAACAAAAGGATCGAATTCAAT 8 GARANGCACCACCACCACACACTATATACAGAGACAAAACAAA		<u>. </u>		
	GATGAAAGCACCAGGATTTCTTATACAGAGGCAAAAACAAAACGATGACGATTCAAT GAAAAGCACCAGGATTTCTTATACAGAGGCAAAAACAAAACGATGGACGATTCAAT GATGAAATCGACAGGTGATACAGAGCAAAATCATTATTGTGCATGCCTATCCGA GATGAAATCGAGCTGATGATTGTGTGTGAGGATAATTGTGTTTTTTTT	CTAGAGGTGGTTAATGACCTCTTTGAAGAACAGACTGAGGAAAATTGTCAAGAAA CTAGAGGTGGTTAATGACCTCTTTGAAGAACAGACTGACCTGGAGAAAATTGTCAAGAAA IIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	26 GATGCCTACCAGGATCCGCGCTTGATCCTTCATCAGCGCTTCCAGTGATCAGT 27 GATGCCTACCAGGATCCGCGCTTTGATCGCTTCCTTTCAGTGATCAGTGATCGCTTTCAGTGATCCGCTTTCAGTGATCCGCTTTCAGTGATCCGCTTTCAGTGATCCGCTTTTCAGTGATCCGATTTTCATTGATCGAGTCCCAATATTTCAGTTTTCATTTTTTTT	026 GCTGAAGTTGACAGCTTAAGGCAGCCACATCGCTGGTGTCAGAACTTGCCATCGAT 110

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ATGCAACATGTTCAAAAGCTGAAGTTGACAAGTTTAAGGCAGCCAACATCCCTCTGGTGT
                           2193 CCCAACTCTATGGAACCTCTGCTACCTTGGAGCATCACCATTTCAACCACGCCGTGATGA
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PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: PCT/EP01/07289
PRIOR FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 20
SOFTWARRE: FastSEQ for Windows Version 4.0
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                          AACGACTTTTTGAGGCTTTTGTCATCTTTTGTGGACTTGGCATCAACACACATTATGT
                                    ATGATCAAGTGAAGAAGTCCTGGGCCCAAGCAGTCTGTGGCTCTTGATGTGCTATCATACC
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Sequence 18, Application US/09891216
Patent No. US20020103120A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INFORMATION:
TITLE OF INVENTION: Regulation of Human
TITLE OF INVENTION: Regulation of Human
TITLE OF INVENTION: Regulation of Human
TITLE OF INVENTION: Phosphodiesterase-Like Enz
FILE REFERENCE: 02973.0051
CURRENT APPLICATION NUMBER: US/09/891,216
CURRENT FILING DATE: 2001-06-26
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/293,221
PRIOR PILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: CT/FEP01/07289
PRIOR APPLICATION NUMBER: CT/FEP01/07289
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
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Pred. No. 0;
0; Mismatches
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Oy 1969 AGTGGGAAGGTACCCAAAACGACTGGTGGCCTCAACTGCCTCATCCTCCTCTG 2028	RESULT 4

Db 399 TTTCAAAGAAAGCATGAGAAAT Qy 686 TGAGCTGGTTGCTTCAACAGGCC	866 866 839 926 899	Oy 986 GGCTCTTGATGTGCTATCATACC					QY .1637
QY 1789 GGGAGGATTAGACTCAAACTCACTCAGCAATTTTTGATCGGAACCGGAAGGATG 1848 Db 3029 GGGAGGATTAGAGCTCAAACTCACTCTTCAGCAATTTTTGATCGGAACCAGTG 1848 Oy 1849 AACTGCCTCGGTTGCAACTGGATGGATTGATGCATTTGATCGATGCATTTTTATCAGCAC 1908 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy 1969 AGTGGGAAGACTACACCAAAAACGACTGCTGGCCTCAACTGCCTCCTCCCCTG 2028	RESULT 5 US-09-891-216-7 Sequence 7, Application US/09891216 ; Patent No. US20020103120A1 ; GENERAL INFORMATION: APPLICANT: Ramakrishnan, Shyam ; TITLE OF INVENTION: Regulation of Human ; TITLE OF INVENTION: Phosphodiesterase-Like Enzyme ; FILE REFERENCE: 02973.00511	CURRENT APPLICATION NUMBER: US/09/891,216 CURRENT FILING DATE: 2001-06-26 PRIOR APPLICATION NUMBER: US 60/213,998 PRIOR FILING DATE: 2000-06-26 PRIOR FILING DATE: 2001-05-25 PRIOR FILING DATE: 2001-05-25 PRIOR FILING DATE: 2001-06-26 PRIOR FILING DATE: 2001-06-26 NUMBER OF SEQ ID NOS: 20 SOFTWARE: FasteEQ for Windows Version 4.0	Score 1664.8; DB 10; Length 2261; Pred. No. 0; O. Tradit 60. Co.	GCAGATGTATCTTCCATTTTGTGGAATCGCCATATCTAACGCTCAGCTCTT 38 [159 TGCTGCCTCAAGGAATATGAAAGAAGCAGAGCTTTGCTAGAGGTTAATGACT 21 446 CTTTGAAGAACAGACTGACCTGGAGAAATTGTCAAGAAATATGCTAGGGCCCAAAC 50 417 [11] [11] [11] [11] [11] [11] [11] [1	QY 566 GAAATTTACCAAATCCTTGAATTGATGTCCCCAAAGTGCAGTGCTGATGCTGAGAACAG 625 Db 339 GAAATTTACCAAATCCTTTGAATTGATGTCCCCCAAAGTGCAGTGCTGATGCTGAGAACAG 398 QY 626 TTTCAAAGAAAGCATGGAGAAATCATCATACTCCGACTGGCTAATAAATA

1345 1645 CCACAACTGGAGACATGCCTTCAACGTGTGTCAGCTGAT 1285 1705 CCATGCAACATGTTCAAAAGCTGAAGTTGACAAGTTTAA 1045 TATGAGACACTGTGTAGGTGGCTTTTGACAGTGAGGAA 1225 CATGACCTCGACCACAGGGGAACCAACAATGCCTTCCA 1405 CATGACCTCGACCACAGGGAACCAACAATGCCTTCCA 1178 SGCCCAACTCTATGGAACCTCTGCTACCTTGGAGCATCA 1465 GCCCCAACTCTATGGAACCTCTGCTACCTTGGAGCATCA 1238 CTTATGCAGCTTTTGAAGCAGTCAATATTGGCAACAGA 1585 CGTGATATATTCGATCAATGTTAATGACAGGAGATA 1478 STCAGAACTTGCCATCGATGACATTCATTTTGATGACTT 1105 MATCACAGCTGCTCTCCGGATGTTCATGGAGCTGGGGAT 1165 938 ATCATCATACTCCGACTGGCTAATAAATAACAGCATTGC 458 745 518 805 578 865 638 925 698 878 SATATCTGGTTTTCACATAAGATCTGTTCTTTGTGTCCC GATATCTGGTTTTCACATAAGATCTGTTCTTTGTGTCCC **AATAATTGGAGTGGCTCAAGTGTTAAACAGACTTGATGG** SAGAACTGAATTCTTTGAACTTGTCAGTAA----------AGGAGAATA GGGTTTCAAGACATTCTGACCGAGGTGGAAATTTTAGC CGTGATATATTCGATCAATGTTAATGACAGCCTGTGA

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Qy 1706 CCTTGGAGCCGTGACCAACCGTGGGAGATCTCCAGACAGGGGGCGCACAACTTGTAAN IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	ACTTGTAACCAG 1765	797 IIGIOLOCO ATTIOGRAFIACCAACCAACCAATAATIGGAGIGGCICAAGIT 	
1766	CAAT 182	857 ACTTGATGGGAAACCTTTTGATGATGAGAACCAACGACTTTTTGAGGCTTTTGTCATCTT	TTTGAGGCTTTTGTCATCTT 916
1826	GCAT 18	917 TTGTGGACTTGGCATCAACAACACAATTATGTATGATCAAGTGAAGAAGTCCTGGGCCAA 	TTGAAGAAGTCCTGGCCAA 976
1886	CCAT 1/1 TAGA 194 	977 GCAGTCTGTGGCTCTTGATGTGCTATCATACCATGCAACATGTTCAAAAGCTGAAGTTGA 	GTTCAAAAGCTGAAGTTGA 1036
1946	CCTC 200	1037 CAAGTTTAAGGCAACCAACATCCCTCTGGTGTCAGAACTTC	GGTCTCAGAACTTGCCATCGATGACATTCATT 1096
2006	AA 2063	1097 TGATGACTTTTCTCCGACGTTGATGCCATGATCACAGCTC	CACAGCTGCTCTCCGGATGTTCATGGA 1156
SULT 6	AA 103	1157 GCTGGGGATGGTACAGAAATTTAAAATTGACTATGAGACAC 	GACACTGTGTAGTGGCTTTTGAC 1216
Sequence 2, Application US/10094168B Publication No. US20030092156A1 GENERAL INFORMATION:	da da	1217 AGTGAGGAAAAACTATCGGATGGTTCTATACCACAACTGGAGACATGCCTTCAACGTGT(AGACATGCCTTCAACGTGTG 1276
APPLICANT: Lanfear, Jerry; Fawcett, Lindsay APPLICANT: Lanfear, Jerry; Fawcett, Lindsay APPLICANT: Bandman, Olga TITLE OF INVENTION: ANTIBODIES SPECIFICALLY BINDING CYCLIC NUCLEOTI	NUCLEOTIDE PDES Db	1277 TCAGCTGATGTTCGCGATGTTAACCACTGCTGGGTTTCAAGACATTCTGACCGAGGTGGA 	SACATTCTGACCGAGGTGGA 1336
FILE ALFERENCE: FF 0.023 2 CLF CURRENT APPLICATION NUMBER: US/10/094,168B CURRENT FILING DATE: 2002-11-13 PRIOR APPLICATION NUMBER: US 09/595,514 DEFORE FILING DATE: 2000-06-14	dd da	1337 AATTTTAGCGGTGATTGTGGGATGCCTGTGTCATGACCTCGACCAGGGGAACCAACAA	BACCACAGGGAACCAACAA 1396
FRIOR FILING DATE: 2007-14 PRIOR FILING DATE: 1999-01-07 NUMBER OF SEQ ID NOS: 7	da .	1397 IGCCTTCCAAGCTAAGAGGCTCTGCCCTGGCCCAACTCTATGGAACCTCTGCTACCTT	FATGGAACCTCTGCTACCTT 1456
SECTION: FIND FIGGRAM ENGTH: 1784 TYPE: DAR ODANIEW HOMO CONIGER	da .	1457 GGAGCATCACCATTTCAACCACGCCGTGATGATCCTTCAAAGTGAGGGTACTTTTTTTT	AGTGAGGGTCACAATATCTT 1516
FEATURE: NAME/KEY: misc_feature OTHER INFORMATION: Incyte ID No. US20030092156A1 HSPDE10A1 S-10-094-168B-2	vo da	1517 TGCTAACCTGTCCTCCAAGGAATATAGTGACCTTATGCAGCTTTTGAAGCAGTCAATATT 	TTTTGAACCAGTCAATATT 1576
; Length	0.784; 0.784; 0.84 0.84 0.84 0.84 0.84 0.84 0.84 0.84	1577 GGCAACAGACCTCACGCTGTACTTTGAGAGGAGAACTGAATTCTTTGAACTTGTCAGTAA	TTCTTTGAACTTGTCAGTAA 1636
TACCAAATCCTTTGAATTGATGTCCC	ATGC 61	1637 AGGAGAATACGATTGGAACATCAAAAACCATCGTGATATATTTCGATCAATGTTAATGAC 	TTTCGATCAATGTTAATGAC 1696
	ATAA 67 	1697 AGCCTGTGACCTTGGAGCGTGACCAAACGTGGGAGATCTCCAGACAGGTGGCAGAACT 	TCCAGACAGGTGGCAGAACT 1756
	ACCA 73	1757 IGTAACCAGTGAGTTCTCGAACAAGGAGATCGGGAGATTAGAGCTCAACTCACTC	TTAGAGCTCAAACTCACTCC 1816
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167	Ξ	1877 TGATAGCATCTGCATGCCTTTGTATCAGGCACTGGTGAAGGTCAACGTGAAA	STCAACGTGAAACTGAAGCC 1936

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APPLICANT: Ramakrishnan, Shyam
TITLE OF INVENTION: Regulation of Human
TITLE OF INVENTION: Phosphodiesterase-Like Enz
FILE REFERENCE: 02973.00511
CURRENT APPLICATION NUMBER: US/09/891,216
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/213,998
PRIOR APPLICATION NUMBER: US 60/293,221
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: CT/EP01/07289
PRIOR APPLICATION NUMBER: PCT/EP01/07289
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SOFWARE: FastSEQ for Windows Version 4.0
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                                                              GCTGGCCTCAACTGCCTCATCCTCCCCTGCCAGTGTTATGGTAGCCAAGGAAGACAG
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APPLICANT: Phillips, Stephen C.; Harrow, Ian
APPLICANT: Landear, Jerry; Fawcett, Lindsay
APPLICANT: Bandman, Jorry; Fawcett, Lindsay
APPLICANT: Bandman, Jorry; Tarrer
TITLE OF INVENTION: ANTIBODIES SPECIFICALLY BINDING CYCLIC NUCLEOTIDE FITLE REFERENCE: PF-0623-2 CIP
CURRENT APPLICATION NUMBER: US/10/094,168B
CURRENT FILING DATE: 2002-11-13
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 1999-01-07
PRIOR FILING DATE: 1999-01-07
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; OTHER INFORMATION: Incyte ID No. US20030092156A1 HSPDE10A2
US-10-094-168B-4
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                                                                                                                                                                                                                                                                                      Sequence 4, Application US/10094168B Publication No. US20030092156A1
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Matches 1048; Conservative
                                                                                                                                                                           GAACTAA 2063
                                                                                                                                                                                              GAACTAA 1623
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SOFTWARE: PERL Program
SEQ ID NO 4
LENGTH: 1982
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US-10-094-168B-4
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Drive
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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S. Wacker
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NAME: NO. US20030054992aland, Greta
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/599,658
FILING DATE: 21-Unn-2000
APPLICATION NUMBER: 09/055,584
FILING DATE: 4-JUNE-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/10/115,515
FILING DATE: 03-Apr-2002
CLASSIFICATION: <UNKNOWN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Marshall, O'Toole, STREET: 6300 Sears Tower, 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                         McAllister-Lucas, Linda
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Beavo, Joseph A. Corbin, Jackie D. Ferguson, Kenneth M. Francis, Sharron H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (312) 474-6300
                                                                                                                                                                                                                                                                                                             ; Sequence 22, Application US/10115515; Publication No. US20030054992A1
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STRANDEDNESS: single
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COMPUTER READABLE FORM:
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STATE: Illinois
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                                Indels
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TITLE OF INVENTION: Regulation of Human
TITLE OF INVENTION: Phosphodiesterase-Like Enzyme
FILE REFERENCE: 02973,00511
CURRENT APPLICATION NUMBER: US/09/891,216
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/293,221
PRIOR APPLICATION NUMBER: 2001-06-26
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 426
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Pred. No. 1.6e-110;
0; Mismatches 2;
99.5%; Pred. No. 1.6e-110;
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Patent No. US20020103120A1
GENERAL INFORMATION:
APPLICANT: Ramakrishnan, Shyam
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Best Local Similarity 99.5's
Matches 390; Conservative
                             390; Conservative
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; ORGANISM: Homo sapiens
US-09-891-216-11
            Best Local Similarity
Matches 390; Conserv
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Thomas, Melissa K.
TITLE OF INVENTION: CAPIC GMP-Specific Phosphodiesterase Materials and Methods
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                                                                                                                                           AGGATCGACGATTCAATGAAATCGACAAGCTGACTGGATACAAGACAAAATCATTAT
                                                                                            TGTGCATGCCTATCCGAAGCAGTGATGGTGAGATTATTGGTGGCCCCAAGCGATAAATA
                                                                                                                                                                             AGATTCCTG---AAGGAGCTCCATTTACTGAAGATGATGAAAAAGTTATGCAGATGTATC
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                                Score 356.6; DB 9;
Pred. No. 6.4e-100;
); Mismatches 854;
NO: 22
SEQUENCE DESCRIPTION: SEQ ID
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0
                                 Query Match 17.2%;
Best Local Similarity 52.0%;
Matches 954; Conservative
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US-10-115-515-22
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GAAATTTAAAATTGACTATGAGACACTGTGTGGTGGCTTTTGACAGTGAGGAAAAACTA
                                                                                                  TCGGATG----GTTCTATACCACAACTGGAGACATGCCTTCAACGTGTGTCAGCTGATGTT
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McAllister-Lucas, Linda
Sonnenburg, William K.
Thomas, Melissa K.
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Francis, Sharron H.
Kadlecek, Ann
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Publication No. US20030054992A1
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
Corbin, Jackie D.
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941 AATTATGTATGATCAAGTGAAGAAGTCCTGGGCCCAAGCAGTCTGTGGCCTCTTGATGTGCT 1000
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                         AATCATCATACTCCGACTGGCTAATAAATAACAGCATTGCTGAGCTGGTTGCTTCAACAG
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INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific Phosphodiesterase Materials and Methods
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                                                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMMUTER: IEM PC compatible
COMMUTER: DatentIn Pelease #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/115,515
FILING DATE: 03-Apr-2002
CIASSIFICATION: «Unknown>
PRIOR APPLICATION ACURROWN>
PRIOR APPLICATION NUMBER: US/09/59,658
FILING DATE: 21-Jun-2000
FILING DATE: 21-Jun-2000
APPLICATION NUMBER: US/09/055,584
FILING DATE: 4-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: NO. US/20030054992Aland, Greta E.
REGISTRATION NUMBER: 35,302
RECERENCE/DOCKET NUMBER: 35,302
RECERENCE/DOCKET NUMBER: 35,302
TELEFORMUNICATION INFORMATION:
TOTAL TO
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S. Wacker
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.larity 52.3%; Pred. No. 1.9e-96;
Conservative 0; Mismatches 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-115-515-12
                                  NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole,
STREET: 6300 Sears Tower, 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1982 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
                                                                                                                    CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 25-3856
                                                                                                                                                                                        ZIP: 60606
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918; Conserv
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Best Local S.
Matches 918
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1649 TTGGAACATCAAAAACCATCGTGATATTTTCGATCAATGTTAATGACAGCCTGTGACCT 1708
                         1727 TTTGGAAGATCCTCATCAAAAGGAGTTGTTTTTGGCAATGCTGATGACAGCTTGTGATCT 1786
                                                   1709 TGGAGCCGTGACCAAACCGTGGGAGATCTCCAGACAGGTGGCAGAACTTGTAACCAGTGA 1768
                                                                 1829 TGATCGGAACCGGAAGGATGAACTGCCTCGGTTGCAACTGGAGTGGATTGATAGCATCTG 1888
                                                                                                                                                                     Sonnenburg, William K.
Thomas, Melissa K.
INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
Phosphodiesterase Materials and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STRET: 6300 Sears Tower, 233 S. Wacker Drive CITY: Chicago STATE: Illinois COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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NAME: No. US20030054992Aland, Greta E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/599,658
FILING DATE: 21-Unn-2000
APPLICATION NUMBER: 09/055,584
FILING DATE: 4-UONE-1998
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REFERENCE/DOCKET NUMBER: 32706
                                                                                                                                                                                                                                                                                                                                      APPLICANT: Beavo, Joseph A.
Corblin, Jackie D.
Ferguson, Kenneth M.
Francis, Sharron H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/10115515 Publication No. US20030054992A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 4474 base pairs
                                                                                                                                                                                                       Kadlecek, Ann
Loughney, Kate
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STRANDEDNESS: single
TOPOLOGY: linear
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US-10-115-515-9
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                                                                                                                                                                                   Score 343.6; DB 9;
Pred. No. 1.1e-95;
0; Mismatches 854;
                                                                                                       ; SEQUENCE DESCRIPTION: SEQ ID NO: US-10-115-515-9
                                                                                                                                                                                   16.5%;
52.0%;
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Best Local Similarity 52.0
Matches 953; Conservative
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MOLECULE TYPE:
                                                   NAME/KEY:
                                                                                 LOCATION:
                             FEATURE
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CURRENT FILING DATE: 1999-05-27

EARLIER APPLICATION NUMBER: 9826777.6

EARLIER FILING DATE: 1998-12-04

EARLIER FILING DATE: 1998-10-30

EARLIER FILING DATE: 1998-10-30

EARLIER APPLICATION NUMBER: 9811500.9

EARLIER APPLICATION NUMBER: 9901247.1

EARLIER PAPLICATION NUMBER: 9901801.1

EARLIER FILING DATE: 1998-04-09

EARLIER FILING DATE: 1998-04-09

EARLIER FILING DATE: 1999-05-10

NUMBER OF SEQ ID NOS: 19

SOFTWARE: PATENTIN VEY: 2.1
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:al Similarity 50.8%;
667; Conservative (
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US-09-321-801-1
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Best Local S
Matches 667
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Patent No. US20020113176A1
APPLICANT: Lanfear, Jeremy
APPLICANT: Lanfear, Jeremy
APPLICANT: Robas, NICOla M.
TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES
FILE REFERENCE: PC9477A
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                                                                 Gaps
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Score 219.2; DB 10;
Pred. No. 4.7e-57;
0; Mismatches 623;
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Pred. No. 5.1e-57;
0; Mismatches 623;
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CURRENT APPLICATION NUMBER: US/09/321,801
CURRENT FILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: 9826777.6
EARLIER FILING DATE: 1998-12-04
EARLIER FILING DATE: 1998-12-04
EARLIER FILING DATE: 1998-10-30
EARLIER FILING DATE: 1998-00-28
EARLIER FILING DATE: 1998-00-09
EARLIER FILING DATE: 1999-00-10
NUMBER: OF SEQ ID NOS: 19
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NUMBER: PATENTING VET: 1399-05-10
NUMBER: PATENTING VET: 1309-05-10
NUMBER: PATENTING VET: 2.1
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Patent No. US20020115176A1
GENERAL INFORMATION:
APPLICANT: Lanfear, Jeremy
APPLICANT: Robas, Nicola M.
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US-09-321-801-3
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AATTGAGAAAGGAATTGCTGGCCAAGTAGCAAGAACAGGGGAAGTCCTGAACATTCCAGA
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1388 AACCAACAATGCCTTCCAAGCTAAGAGTGGCTCTGCCCTGGCCCAACTCTATGGAACCTC 1447
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 1449 AATTGAATTATTCCACTTTGACATTGGTCCTTTTGAAAACATGTGGCCTGGAATTTTTGT 1508
                                                              1509 CTACATGGTTCATCGGTCCTGTGGGACATCCTGCTTTGAGCTTGAAAAGTTGTGTCTTT 1568
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2321 GGCAAATGATATATGCAGAATTCTGGGCTGAGGGTGAT---GAAATGAAGAAATTGGG 2377
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Patent No. US20020081633A1
GENERAL INFORMATION:
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Hunter, John Joseph
APPLICANT: Hunter, John Joseph
APPLICANT: Hulliamson, Mark
TITLE OF INVENTION: Methods for Using 22045, A Huma
TITLE OF INVENTION: Nucleotide Phosphodiesterase
FILE REPERENCE: 5800-71
CURRENT APPLICATION NUMBER: US/09/420,190
CURRENT FILING DATE: 1999-10-18
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
SSOFTWARE: 4381
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10.5%; Score 217.6; DB 10;
Best Local Similarity 50.7%; Pred. No. 2.2e-56;
Matches 666; Conservative 0; Mismatches 624;
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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 protein search, using sw model OM protein

June 13, 2003, 15:44:04; Search time 45.1845 Seconds (without alignments) 3119.127 Million cell updates/sec Run on:

US-09-663-542-1

Perfect score:

1 MLKQARRPLFRNVLSATQWK.....ASTASSSSPASVMVAKEDRN'684 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 Total number of hits satisfying chosen parameters: 671580 segs, 206047115 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

sp_fungi:* sp_human:* sp_invertebrate:* SPTREMBL_21:*
: sp_archea:*
: sp_bacteria:* sp_mammal:*

sp_unclassified:* sp_virus:*
sp_vertebrate:* sp_rvirus:*
sp_bacteriap:* sp_archeap:* sp_plant:* sp_rodent:*

sp_organelle:* sp_phage:*

sp_mhc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ				
Result No.	Score	Query Match	Ouery Match Length DB	DB	ID .	Description
	3516	100.0	684	4	09G2Y7	Ogazy7 homo sapien
7	3354	95.4	988	4	096876	096s76 homo sapien
3	3294:5	93.7	685	11	70IV90	O8vid7 rattus norv
4	3250	92.4	934	4	O9HCR9	Ogher9 homo sanien
2	3117.5	88.7	935	11	08VID6	O8vid6 rattus norv
9	2970	84.5	576	4	09нв46	Oghb46 homo sapien
7	2845.5	80.9	581	Π	08VID8	O8vid8 rattus norv
80	2541	72.3	490	4	Q9NY45	O9nv45 homo sapien
6	1511.5	43.0	1284	2	62579	09vi79 drosophila
10	1478	42.0	1018	2	095TW8	095tw8 drosophila
11	1380.5	39.3	1232	2	09VF19	Ogvfi9 drosophila
12	1054.5	30.0	861	11	091201	O91zgl mus musculu
13	1021	29.0	857	13	Q8UUY6	O8uuv6 rana pipien
14	1019.5	29.0	861	13	QBUUY5	O8uuy5 rana pipien
15	1017	28.9	866	13	Q8UUY7	O8uuv7 rana pipien
16	866	28.4	856	9	09MYV0	O9mvv0 canis famil

7 mus 4 mus	Q9htv4 homo sapien Q9htp9 homo sapien	Q9UIW9 NOMO Sapien O96076 ephydatia f	Q9wvil mus musculu	Q9qyj5 rattus norv	Q9qyj6 rattus norv	Q9gqu6 trypanosoma	Q8wqx9 trypanosoma	097746 canis famil	Q9gtn9 trypanosoma	Q9qwh9 rattus norv	Q8qzv1 rattus norv	076105 homo sapien	043849 homo sapien	Q9upj5 homo sapien	043850 homo sapien	P78505 homo sapien	Q9egr7 rattus norv	Q8r078 mus musculu	Q9h3h2 homo sapien	089084 mus musculu	035470 rattus norv	Q9vke9 drosophila	P94181 anabaena sp	Q8sxr0 drosophila	Q8vie3 rattus norv
Q62037 Q8R0D4	09NTV4 09HCP9	Q901W9	Q9WVI1	090175	090YJ6	09GQU6	O8WQX9	097746	O9GTN9	6HM060	Q8QZV1	076105	043849	Q9UPJ5	043850	P78505	Q9EQR7	Q8R078	09н3н2	089084	035470	Q9VKE9	P94181	Q8SXR0	Q8VIE3
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ALIGNMENTS

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MEDLINE=20469516; PubMed=10906126;
Yuasa K., Kotera-J., Fujishige K., Michibata H., Sasaki T., Omori K.;
Yuasa K., Kotera-J., Fujishige K., Michibata H., Sasaki T., Omori K.;
Tsolation and Characterization of Two Novel Phosphodiesterase PDE11A
Variants Showing Unique Structure and Tissue-specific Expression.";
J. Biol. Chem. 275:31469-31479(2000).
EMBL, AA2786682; CAC15567.1;
EMBL, AA3786682; CAC15567.1;
InterPro; IPR003607; ME_Pplase_HDc.
InterPro; IPR003607; ME_Pplase_HDc.
InterPro; IPR003607; PDEase.
Pfam: PF01590; GAP:
Pfam: PF01590; GAP:
Pfam: PF01231; PDEase; 1.
                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MNN-2002 (TrEMBLrel. 11, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
0AMP/OGMP cyclic nucleotide phosphodiesterase 11A3 (Phosphodiesterase
                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=20524097; PubMed=11050148;
MEDLINE=20524097; PubMed=11050148;
Hetman J.M., Robas N.M., Baxendale R., Fidock M., Phillips S.C.,
Soderling S.H., Beavo J.A.;
Cloning and characterisation of two splice variants of human
phosphodiesterase 11A.";
Proc. Natl. Acad. Sci. U.S.A. 97:12891-12895(2000).
                                      684 AA
                                      PRT;
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SMART; SM00065; GAF; 2.
                                      PRELIMINARY;
                                                                                                                                                                           PDE11A3 OR HSPDE11A
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RESULT 1
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AB048422;
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                                                                                                          SNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCERCSVLLLED 180
                                                                                                                                                                                                  AYQDPRFDAEADQISGFHIRSVLCVPIWNSNHQIIGVAQVLNRLDGKPFDDADQRLFEAF 300
                                                                                                                                                                                                                                 VIFCGLGINNTIMYDQVKKSWAKQSVALDVLSYHATCSKAEVDKFKAANIPLVSELAIDD 360
                                                                                                                                                                                                                                          IHFDDFSLDVDAMITAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLYHNWRHAF 420
                                                                                                                                                                                                                                                                            NVCQLMFAMLTTAGFQDILTEVEILAVIVGCLCHDLDHRGTNNAFQAKSGSALAQLYGTS 480
                                                                                                                                                                                                                                                                                                          099
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                                                                                                                                         1 MLKQARRPLFRNVLSATOWKKVKITRLVQISGASLAEKQEKHQDFLIQRQTKTKDRRFND
                                                                           MLKQARRPLFRNVLSATQWKKVKITRLVQISGASLAEKQEKHQDFLIQRQTKTKDRRFND
                                                                                                                                                                                                                                                                                                                                  ATLEHHHFNHAVMILQSEGHNIFANLSSKEYSDLMQLLKQSILATDLTLYFERRTEFFEL
                                                                                                                                                                                                                                                                                                                                                                  VSKGEYDWNIKNHRDIFRSMLMTACDLGAVTKPWEISRQVAELVTSEFFEQGDRERLELK
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                                                                                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
                                                 0;
                                Length 684;
                                                 Indels
        PDEASE_I; 1.
; 78133 MW; 1E41C4F5199D6B1E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata;
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Created)
Last sequence update)
Last annotation update)
                               100.0%; Score 3516; DB 4;
100.0%; Pred. No. 3.5e-253;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             988 AA
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MEDLINE=20570133; PubMed=11121118;
Yuasa K., Kanoh Y., Okumura K., Omori
                                                                                                                                                                                                                                                                                                                                                                                                                                            KRLLASTASSSPASVMVAKEDRN 684
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Eukaryota, Metazoa; Chordata; Cr Mammalla; Eutheria; Primates; Ca
                                       al Similarity 100.
684; Conservative
SMART; SM00471; HDc; 1.
PROSITE; PS00126; PDEAS
                684 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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Q96S76;
                                         Best Local
Matches 68
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Q96S76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 PTAIDYKCHLKKHNERQFFLELVKDISNDLDLTSLSYKILIFVCLMVDADRCSLFLVEGA 300
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Pred. No. 6.7e-241;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00126; PDEASE_I; UNKNOWN_
                                                         with other
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                                                                                                                                                                                                                                                                                                                                            BAB62713.1; j
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BAB62713.1;
BAB62713.1;
BAB62713.1;
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BAB62713.1;
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BAB62713.1;
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BAB62713.1;
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InterPro; IPR002073; PDEase
                                                                                                                                                                                                     BAB62713.1
BAB62713.1
BAB62713.1
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Pfam; PF00233; PDEase;
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Matches 684; Conserv
                                                                                                                                                                                                                                                                                                   AB048404; EAB048405; EAB048406; EAB048408; EAB048408; EAB048408; EAB048409; EAB04869; EAB04869; EAB04969; EAB0409; EAB04969; EAB04969; EAB04969; EAB04969; EAB04969; EAB04969; E
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AB048411;
AB048412;
AB048413;
                                                                                                                                                                                                          AB048402;
                                                                                                                                                                                                                                                    AB048403;
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us-09-663-542-1.rspt

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240

300 300

240

360 360 420 420 480 480 540 540 900

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EIDKLFGYKTKSLLCMPIRNSDGEIIGVAQAINKVPEGAPFTEDDEKVMQMYLPFCGIAI 120
                                                      AYQDPRFDAEADQISGFHIRSVLCVPIWNSNHQIIGVAQVLNRLDGKPFDDADQRLFEAF
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MEDLINE=20469516; PubMed=10906126;
MEDLINE=20469516; PubMed=10906126;
Vuasa K., Kotera J., Fujishige K., Michibata H., Sasaki T., Omori K.;
Viasa K., Kotera J., Fujishige K., Michibata H., Sasaki T., Omori K.;
Viasa K., Kotera J., Fujishige K., Michibata H., Sasaki T., Omori K.;
Variants Showing Unique Structure and Tissue-specific Expression.";
J. Blol. Chem. 275:31469-31479(2000).
                                                                                                                                                               IESPVVKFTKSFELMSPKCSADAENSFKESMEKSSYSDWLINNSIAELVASTGLPVNISD
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GAF domains.";
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Yuasa K., Kanch Y., Okumura K., Omori K.;
"Genomic organization of the human phosphodiesterase PDE11A i
Evolutionary relatedness with other PDEs containing GAF doma
Eur. J. Biochem. 268:168-178(2001).
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1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 11, Last annotation update)
Phosphodiesterase 11A (Phosphodiesterase 11A4).
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EMBL; AB036704; BAB16371.1;
EMBL; AB048423; BAB62712.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                   FEAFVIFCGLGINNTIMYDQVKKSWAKQSVALDVLSYHATCSKAEVDKFKAANIPLVSEL
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X WEDLINE=21393948; PubMed=11502204;
Yuasa K., Ohgaru T., Asahina M., Omori K.;
T "Identification of rat cyclic nuclectide phosphodiesterase 11A
T (PDE11A): comparison of rat and human PDE11A splicing variants.";
T ENT. J Biochem. 268:4400.4448(2001).
R EMBL; AB059361; BA879628.1;
R InterPro; IPR003018; GAF.
R InterPro; IPR002018; PDEase.
R Pfam: PF01590; GAF; 2.
R Pfam: PF01590; GAF; 2.
R PRINTS; PR00387; PDIESTERASE1.
R PRINTS; PR00387; PDIESTERASE1.
R PRINTS; PR00387; PDIESTERASE1.
R SMART; SM00471; HDC; 1.
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Sciurognathi; Muridae; Murinae; Rattus.
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78067 MW; 505E8748E9A6C21F CRC64;
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                             Yusas K., Ohgaru T., Asahina M., Omori K.;
Yusas K., Ohgaru T., Asahina M., Omori K.;
"Identification of rat cyclic nucleotide phosphodiesterase 11A
"Identification of rat and human PDE11A splicing variants.";
Eur. J. Biochem. 268.4440-4448(2001).
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SMART; SM00471; HDC; 1.
PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
SEQUENCE 935 AA; 104570 MW; E80F1039770F8276 CRC64;
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Pred. No. 2.5e-223;
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InterPro; IPR003018; GAF.
InterPro; IPR002073; PDEase.
Pfam; PF01590; GAF; 2.
Pfam; PF00233; PDEase; 1.
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MEDLINE=21393948; PubMed=11502204;
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01-MAR-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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; 104810 MW; 994675824259447E CRC64;
                                                                                                                                                                                                                                                                                                                92.4%; Score 3250; DB 4; 99.8%; Pred. No. 3.4e-233; ive 1; Mismatches 0;
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Interpro; IPR003607; ME_Pplase_HDc
InterPro; IPR002073; PDEase.
                                                                                                                                                                                                                                                  PRINTS; PR00387; PDIESTERASE1
           BAB62712.1;
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Pfam; PF00233; PDEase; 1
                                                                                                                                                                                                                                                              SMART; SM00065; GAF; 2
SMART; SM00471; HDc: 1
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ABO48403;
ABO48404;
ABO48405;
ABO48406;
ABO48409;
ABO48410;
ABO48411;
ABO48411;
ABO48411;
ABO48411;
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AB048415;
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AB048419;
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AB048417;
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Best Local Si
Matches 630;
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LKCERCSVLLLEDIESPVVKFTKSFELMSPKCSADAENSFKESVEKSSYSDWLINNSIAE 123
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                                                                                                                     RMVLYHNWRHAFNVCQLMFAMLTTAGFQD1LTEVE1LAV1VGCLCHDLDHRGTNNAFQAK
                                                         SGSALAQLYGTSATLEHHHFNHAVMILQSEGHNIFANLSSKEYSDLMQLLKQSILATDLT
                                                                                                                                                                                                      FEQGDRERLELKLIPSAIFDRNRKDELPRLQLEWIDSICMPLYQALVKVNVKLKPMLDSV
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MEDLINE-21993948; PubMed=11502204;
Yuasa K., Ohgaru T., Asahina M., Omori K.;
Yuasa K., Ohgaru T., Asahina M., Omori K.;
Yuasa K., Ohgaru T., Asahina M., Omori K.;
Tedentification of rat cyclic nucleotide phosphodiesterase 11A
(PDE11A): comparison of rat and human PDE11A splicing variants.";
Eur. J. Biochem. 268:4440-4448(2001).
EmBL; AB059360; BAB79627.1; -.
InterPro; IPR003607; GAF.
InterPro; IPR003607; PDEase.
InterPro; IPR002073; PDEase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.9%; Score 2845.5; DB 11; Length 581; larity 95.7%; Pred. No. 2.2e-203; Conservative 6; Mismatches 12; Indels 7;
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CA7C2F5DDB37D00 CRC64;
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581 AA; 66141 MW;
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Pfam; PF00233; PDEase; 1
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nes 555; Conserv
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01-MAR-2002
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                                        RERLELKLTPSA1FDRNRKDELPRLQLEWIDSICMPLYQALVKVNVKLKPMLDSVATNRS
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hetman J.M., Robas N., Baxendale R., Fidock M., Phillips S.C., Soderling S.H., Beavo J.A.; Baxendale R., Fidock M., Phillips S.C., Soderling and characterization of two splice variants of human phosphodiesterase 11A.";

Proc. Natl. Acad. Sci. U.S.A. 97:12891-12895(2000).

BMBL; AF281865, AAG32023.1;

InterPro; IPR003667; ME_Pplase_HDc.

InterPro; IPR003607; ME_Pplase_HDc.

InterPro; IPR003607; ME_Pplase_HDc.

Pfam; PF01530; PDEase.
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Last annotation update)
11A2.
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100.0%; Pred. No. 1.2e-212;
ive 0; Mismatches 0;
                                                                                                                                                                                KWEELHQKRLLASTA----SSSSPASVMVAKEDR 683
                                                                                                                                                                                                      576 AA
                                                                                                                                                                                                                                                                                                                                                                   Created)
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MEDLINE=20524097; PubMed=11050148;
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Mammalia; Eutheria; Primates;
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SMART; SM00065; GAF; 1.
SMART; SM00471; HDC; 1.
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576 AA; 65766 MW;
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nes 576; Conservative
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Matches 576
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NCBI_TaxID=7227;
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ANIPLVSELAIDDIHFDDFSLDVDAMITAALRMFMELGMVQKFKIDYETLCRWLLTVRKN 303
                                                                                                                                            YRMVLYHNWRHAFNVCQLMFAMLTTAGFQDILTEVEILAVIVGCLCHDLDHRGTNNAFQA
                                     YRMVLYHNWRHAFNVCOLMFAMLTTAGFOEILTEVEILAVIVGCLCHDLDHRGTNNAFOA
                                                       KSGSALAQLYGTSATLEHHHFNHAVMILQSEGHNIFANLSSKEYSDLMQLLKQSILATDL
                                                                                           TLYFERRTEFFELVSKGEYDWNIKNHRDIFRSMLMTACDLGAVTKPWEISRQVAELVTSE
                                                                                                                                 FFEQGDRERLELKLTPSAIFDRNRKDELPRLQLEWIDSICMPLYQALVKVNVKLKPMLDS
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Yuasa K., Kanoh Y., Okumura K., Omori K.;
"Genomic organization of the human phosphodiesterase PDE11A gene:
Evolutionary relatedness with other PDEs containing GAF domains.";
Eur. J. Biochem. 268:168-178(2001).
                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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BEDLINE-20202699; PubMed-10725373;
Fawcett L., Bacandale R., Stacey P., McGrouther C., Harrow I Soderling S., Hetman J., Beavo J.A., Phillips S.C.;
"Molecular cloning and characterization of a distinct human phosphodiesterase gene family:PDEIAA.";
Physphodiesterase gene family:PDEIAA.";
Proc. Natl. Acad. Sci. U.S.A. 97:3702-3707(2000).
                                                                                                                                                                      VATNRSKWEELHQKRLLASTA----SSSSPASVMVAKEDR 683
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Mammalia; Eutheria; Primates;
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AB048408; BAB62714.
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AB048412;
AB048413;
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Bukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                         Length 490;
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100.0%; Pred. No. 8.1e-181;
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Mismatches
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PRINTS; PR00387; PDIESTERASE1
SMART; SM00065; GAF; 1.
SMART; SM00471; HDC; 1.
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RA Berson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Bouck J., Brokstein P., Brottler P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delloher A., Deng Z., Mays A.D., Daw I., Dietz S.M.,
RA Dodson K., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Fosler C., Gabrielian A.E., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Alali M., Kalush F., Karpen G.H., Re Z., Kennison J.R., Ketchum K.A.,
RA Alali M., Kalush F., Karpen G.H., Re Z., Kennison J.A., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Nelson D.R., Nelson K.A., Nixon K., Nixsken D.R., Parle D.L.,
RA Reinert K., Remington K., Sunders R.D.C., Scheeler F., Shen H.,
RA Shier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Wang Z.-Y., Wassarman D.A., Weinstchoff M., Welssenbach J.,
RA Alliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Cheng X. H., Zhong F.N., Zhong K., Zhu S., Zhu X., Smith H.O.,
RA Cheng X. H., Myers E.W., Rubin G.M., Venter J.C.;
RA Cheng Sequence of Drosophila melanogaster.";
R. Science 287:2185-2195(2000).
R. Physics F. Physics F. W., Shill M., Shill R., Shill 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 SPVVKFTKSFELMSPKCSADAENSFKESMEKSSYSDWLINNSIAELVASTGLPVNISDAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    442 KG--SFSRVFDFEANDLSEEEATSRTSPYE----SRFPINIGITGHVATTGETVNVPNAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---KTKDRRFNDEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.0%; Score 1511.5; DB 5; Length 1284;
44.4%; Pred. No. 1.4e-103;
Live 126; Mismatches 202; Indels 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FCGLGINNTIMYDQVKKSWAKQSVALDVLSYHATCSKAEVDKF -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART: SM00065; GAF; 2.
SMART: SM00471; HDC; 1.
PROSITE: P00126; PDBASE_I; 1.
SEQUENCE 1284 AA: 141726 MW; F6873C90A9953430 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 KKVKITRLVQISGASLAEKQEKHQDFLIQRQT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003018; GAF.
InterPro; IPR003607; ME_Pplase_HDc.
InterPro; IPR002073; PDEase.
Pfam; PF0159; GAF. 2.
Pfam; PF00233; PDEase; 1.
PRINTS; PR00387; PDIESTERASE1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FlyBase; FBgn0032686; CG10231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243
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SLPPRKKLQRRLRVPSAVHFRLHDFKFDDIHFEDDDTLKACLRMFLDLDFVERFHIDYEV 675
                                                                                                    DHRGTNNAFQAKSGSALAQLYGTSATLEHHHFNHAVMILQSEGHNIFANLSSKEYSDLMQ 516
                                                                                                                                                                                                                                                                                                                                                                               SRQVAELVTSEFFEQGDRERLELKLTPSAIFDRNRKDELPRLQLEWIDSICMPLYQALVK 636
                                                                                                                                                                                                                                                                                                                                                                                                              88 VAQAINKIPEGAPFTEDDEKVMQMYLPFCGIAISNAQLFAASRKEYERSRALLEVVNDLF 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               517 LLKQSILATDLTLYFERRTEFFELVSKGEYDWNIKNHRDIFRSMLMTACDLGAVTKPWEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 VQISGASLAEKQEKHQDFLIQRQTKTKDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                            LCRWLLTVRKNYRMVLYHNWRHAFNVCQLMFAMLTTAGFQDILTEVEILAVIVGCICHDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AV56470; AAL13699.1; --
Flybase; FBgn0038237; CG8279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1018;
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InterPro; IPR001230; Prenyl_site.
Pfam; PF01590; GAF; 2.
Pfam; PF00233; PDEase; 1.
PROSTTE; PS000126; PDEASE_I; UNKNOWN_1.
PROSTTE; PS00294; PRENYLATION; UNKNOWN_1.
SEQUENCE 1018 AA; 114668 MW; 8C758A607855EDD9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Last annotation update)
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3.1e-101;
ches 208;
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LSDKLEPLVEGVRDNRGHWIDL 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VNVKLKPMLDSVATNRSKWEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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A Manatides P.G., Scherer S.E., Holf R.A., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Holf W., Hoskins R.A., Galle R.F.,
A George R.A., Lewis S.E., Sichards S. Ashburner M., Henderson S.N.,
A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Brandon R.C., Bayer E.G., Hell G., Nelson C.R., Miklos G.L.G.,
A Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
A Beleson K.Y., Bencos P.V., Berman B.P., Bhandari D., Boshakov S.,
A Borkova D., Botchan M.R., Bouck J., Brokstein P., Botcher P.,
A Borkova D., Botchan M.R., Bouck J., Brokstein P., Botcher P.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
A Durbin K.J., Evangelista C.C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Gargn N.S., Gelbart W.M., Glasser K.,
                                                                                                                                                                                                 618
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                                                                                                                                                                                                                                      LMSPKCSADAENSFKESMEKSSYSDWLINNSIAELVASTGLPVNISD
                            SIFEAFAIFCGLGIHNTQMYENACKLMAKQKVALECLSYHATASQDQTEKLTQDVIAEAE
                                                                                                                                                                                    SYNLYSFTFTDFELVDDDTCRAVLRMFMQCNLVSQFQIPYDVLCRWVLSVRKNYRPVKYH
                                                                                                                                                                                                                                                                                            535 TEFFELVSKGEYDWNIKNHRDIFRSMLMTACDLGAVTKPWEISRQVAELVTSEFFEQGDR
                                                                                                                                                                                                                                                                                                                                               ERLELKLTPSAIFDRNRKDELPRLQLEWIDSICMPLYQALVKVNVKLKPMLDSVATNRSK
                                                                                                                                                                                                                                                                                                                                                                                                  241 A-----YQDPRFDAEADQISGFHIRSVLCVPIWNSNHQIIGVAQVLNRLDGKPFDDADQ
                                                                                                                  RLFEAFVIFCGLGINNTIMYDQVKKSWAKQSVALDVLSYHATCSKAEVDKFKAANIPLVS
                                                                                                                                                                    ELAIDDIHFDDFSLDVDAMITAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLYH
                                                                                                                                                                                                                          NWRHAFNVCQLMFAMLTTAGFQDILTEVEILAVIVGCLCHDLDHRGTNNAFQAKSGSALA
                                                                                                                                                                                                                                                                             QLYGTSATLEHHHFNHAVMILQSEGHNIFANLSSKEYSDLMQLLKQSILATDLTLYFERR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda: Tracheata: Hexapoda: Insecta;
Pterygota: Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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1-MAR-2001 (TrEMBLrel. 16,
1-JUN-2002 (TrEMBLrel. 21,
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RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Ralush F., Karpen G.H., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Markulov G., Malshina N.V., Mobarry C., Mornis J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Mount S.M., Moy M., Murphy B., Pollard J., Puri V., Reese M.G.,
RA Rahazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Sanders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ve J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang L.,
RA Glabs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RL Genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
REMBL, REDORATOR S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RLFEAFVIFCGLGINNTIMYDQVKKSWAKQSVALDVLSYHATCSKAEVDKFKAANIPLVS 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 VQISGASLAEKQEKHQDFLIQRQTKTKDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VAQAINKIPEGAPFTEDDEKVMQMYLPFCGIAISNAQLFAASRKEYERSRALLEVVNDLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SFEEKKMRNRFTVLFELGGEYQAANVSRPSVSELSSSTLA---QIAQFVATTGQTVNICD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A----YQDPRFDAEADQISGFHIRSVLCVPIWNSNHQIIGVAQVLNRLDGKPFDDADQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NWRHAFNVCQLMFAMLTTAGFQDILTEVEILAVIVGCLCHDLDHRGTNNAFQAKSGSALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---LMSPKCSADAENSFKESMEKSSYSDWLINNSIAELVASTGLPVNISD
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; ECF6B9C3A71BAF74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3e-94;
es 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.3%; Score 1380.5; 38.9%; Pred. No. 7.3e.ive 109; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Firmase; FBGT0038237; CG6279.
InterPro: IPR003018 GAF.
InterPro: IPR0020073; PBCPplase_HDc.
InterPro: IPR0020073; PDEase.
InterPro: IPR001203; Prenyl_site.
Pfam; PF001599; GAF; 2.
Pfam; PF00233; PDEase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00126; PDEASE_I; 1.
PROSITE; PS00294; PRENYLATION; UI
SEQUENCE 1232 AA; 137426 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 38.9%; Pr
nes 299; Conservative 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00387; PDIESTERASE1.
SMART; SM00065; GAF; 2.
SMART; SM00471; HDc; 1.
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Matches
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DVDAMITAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLYHNWRHAFNVCQLMFA 428
                                                                                                                                                                                                                                                           MLTTAGFQDILTEVEILAVIVGCLCHDLDHRGTNNAFQAKSGSALAQLYGTSATLEHHHF 488
                                                                                                                                                                                                                                                                                    546 -----YDWNIKNHRDIFRSMLMTACDLGAVTKPWEISRQVAELVTSEFFEQGDRERLE 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        599 LKLTPSAIFDRNRKDELPRLQLEWIDSICMPLYQALVKVNVKLKPMLDSVATNRSKWEEL 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42 HQDFLIQRQTKTKDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPF 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102 TEDDEKVMQMYLPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIM 161
                                                                                                                                                                                                                                                                                                                                                                              489 NHAVMILQSEGHNIFANLSSKEYSDLMQLLKQSILATDLTLYFERRTEFFELVSKGE---
  517 TEHELVKCGLRLFLEINVVEKFKVPVEVLTRMMYTVRKGYRPVTYHNWRHGFNVGQTMFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
Ranidae; Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    857;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li N., Baehr W.;
"Frog retina PDE6 subunits.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY044175; AAK95400.1;
-InterPro; IPR0033018; GAF.
InterPro; IPR003018; GAF.
InterPro; IPR0015073; PDEase.
InterPro; IPR001230; Prenyl_site.
Pf01590; GAF; 2.
Pfam; PF01590; GAF; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00126; PDEASE_I; UNKNOWN_I.
PROSITE; PS00294; PRENYLATION; UNKNOWN_I.
SEOUENCE 857 AA; 99213 MW; 562B8549E5B650E8 CRC64;
                                                                      SYHATCSKAEVD---KFK-AANIPLVSE----LAI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rana pipiens (Northern Leopard frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228; Conservative 131; Mismatches 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       659 HOKRLLASTASSSSPASVMVAKED 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------8EEYEAKVKVTEEE 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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SMART; SM00065; GAF; 2.
SMART; SM00471; HDC; 1.
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PDE6B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----EGHNIFANLSSKEYSDLMQLLKQSILATDLTLYFERRTEFFELVSKGEYDWNIKNH 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 CSVLLL------EDIESPVVKFTKSFELMSPKCSADAENSF------KESME--KS 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              277 YSIGLLDMTKEKEFYDEWPIKLGEVEPYKGPKTPDGREIIFYKIIDYILHGKEEINVIPS 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 SYSD-WLINNSIAELVASTGLPVNISDAYQDPRFDAEADQI--SGFHIRSVLCVPIWNSN 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         272 HQIIGVAQVLNRLDGKPFDDADQRLFEAFVIFCGLGINNTIMYDQVKKSWAKQSVALDVL 331
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792 ILY-TTSTMEHHHFDHFRLAAFLDRLAAFRRALRDLARELLDLVEELVVDPTLIFLVIEY
                                                                                                                                                                                         TKRTRDNFWLDALSPEDYRSVMKTVESAILSTDLAMYFKKRNAFLELVENGEFDWQGEEK
                                                                                                                                                                                                                                                      RDIFRSMLMTACDLGAVTKPWEISRQVAELVTSEFFEOGDRERLELKLTPSAIFDRNRKD
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                                                                                                                FRLLRRTIFLFEPELDEEDDDVVDSVVDSVVVLSVVLVLDSVLVLLSAALTWATYKTIER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11; Length 861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chang B., Hawes N.L., Hurd R.E., Davisson M.T., Nusinowitz S., Heckenlively J.R.;

"A sequence alteration in Pde6c gene causes cone photoreceptor
                                                                                                                                                                                                                                                                                                                                                                            ELPRLQLEWIDSICMPLYQALVKVNVKLKPMLDSVATNRSKWEELHQK 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lil
SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE=RETINA;
Chanq B., Hawes N.L., Hurd R.E., Davisson M.T., Nusinowitz S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 35.5%; Pred. No. 8.1e-70;
Matches 243; Conservative 130; Mismatches 242; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 function loss (cpfil) in mice.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF411063; AAK96254.1;
MGD; MGI:109556; Pde6c.
InterPro; IPR003018; GAF.
InterPro; IPR0012073; PDEase.
InterPro; IPR001203; Prenyl_site.
Pfam; PF001590; GAF; 2.
Pfam; PF00233; PDEase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PFU1590; una., i. pfam; PFU1590; PDEase; 1. PFAM. 1. PROSITE; PS00126; PDEASE_I; UNKNOWN_1. PROSITE; PS00294; PREWYLATION; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.0%; Score 1054.5; DB 35.5%; Pred. No. 8.1e-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    861 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
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01-JUN-2002
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B8F3A689EA5D7249 CRC64;

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SEQUENCE
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Matches
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                                                                                                                       GFHIRSVLCVPIWNSNHQIIGVAQVLNRLDGKPFDDADQRLFEAFVIFCGLGINNTIMYD
                                                                                                                                  438 KMNKLENRKGIAQDMVMYHVRCNKEEMQDILPSRAKLGKELEQCEEDEIAQLLKKELPGP
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VAAEFWEQGDLERTVLQQQPIPWMDRNKSAELPKPQCGFIDFVCTFVXKEFSRFHEEIQP
                                SPKCSADAENSF - - -
                                                                          -----KESME---KSSYSDWLINNSIAELVASTGLPVNISDAYQDPRFDAEADQI--S
                                                                                               318 IDYILHGKEDIKVIPNPPADHWALISGLPTYVAESGFICNIMNAAADEMFKFQREPLDES
                                                                                                                                                                                                              ---AIDDIHFDDFSLDVDAMITAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLY
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01-JUN-2002 (TEMBLEEL: 21, Last annotation update)
Retinal cone PDE6 alpha' subunit.
Rana pipiens (Northern leopard frog).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi;
Amphibia: Batrachia: Anura: Neobatrachia; Ranoidea; Ranidae: Rano.
NCBI_TaxID=8404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Li N., Baehr W.;
"Frog retina PDES subunits.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY044176; AAK95401.1;
InterPro; IPR003018; GAF.
InterPro; IPR0030018; GAF.
InterPro; IPR002073; PDEAse.
InterPro; IPR002073; PDEAse.
InterPro; IPR001230; Prenyl_site.
Pfam; PP01590; GAF: 2.
                                                                                                                                                                   QVKKSWAKQSVALDVLSYHATCSKAEVDKFKAANIPLVSEL - - -
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Last sequence update)
Last annotation update)
                               HRAQTLLKCERCSVLLLEDIESPVVKFTKSFELM-
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PROSITE; PS00294; PRENYLATION; UNKNOWN_I.
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SMART; SM00065; GAF; 2.
SMART; SM00471; HDC; 1.
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                                                                                                       EYISMVLKKNHINYLYNIELRKSKVMLWCANKVFEELTDIERQFHKALYTVRIYLNCERY
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SKTLLEDETINIFQNLNKRQFENVIHLFEVAIIATDLALYFKKRTMFQKIVDAAEQMQSE
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                                                                                 KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYL
                                          Gaps
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Ranidae; Rana.
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    Length 861;
                                          59;
                                          Indels
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"Frog retina PDE6 subunits.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia: Barrachia; Anura; Neobatrachia; Ranoidea;
NCBL_TaxID=8404;
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    DB 13;
                    .3e-67;
es 248;
29.0%; Score.1019.5; 33.4%; Pred. No. 3.3e.ive 138; Mismatches
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                                        Conservative 138;
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01-JUN-2002 (
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                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 AENSF------KESME---KSSYSDWLINNSIAELVASTGLPVNISDAYODPRFDA 249
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                          InterPro; IPR003018; GAF.

InterPro; IPR003018; GAF.

InterPro; IPR002073; PDEase. HDC.

InterPro; IPR002073; PDEase.

Pfam; PF01590; GAF; 2.

Pfam; PF01580; GAF; 2.

Pfam; PF01580; GAF; 2.

PRINTS; PR00387; PDIESTERASE1.

SMART; SM00065; GAF; 2.

SMART; SM00471; HDC; 1.

PROSITE; PS00126; PDEASE_I; UNKNOWN_1.

PROSITE; PS00126; PDEASE_I; UNKNOWN_1.

PROSITE; PS001294; PRENTLATION; UNKNOWN_1.
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Best Local Similarity 32.9%; Pred. No. 5.1e-67;
Matches 237; Conservative 124; Mismatches 268;
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EMBL; AY044174; AAK95399.1; -.
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Search completed: June 13, 2003, 15:48:48 Job time : 50.1845 secs THIS PAGE BLANK (USPTO)

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein June 13, 2003, 15:45:35 ; Search time 26.4875 Seconds Run on:

(without alignments) 2482.530 Million cell updates/sec

Title: Perfect score:

US-09-663-542-1 3516 1 MLKQARRPLFRNVLSATQWK......ASTASSSSPASVMVAKEDRN 684 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

283224

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

summaries Maximum Match 100% Listing first 45 s Post-processing: Minimum Match 0%

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		dЮ			SUMMARIES	
Result No.	Score	Query	Length	DB	QI	Description
1	. 99	· œ	7	-	JW0106	-
7	355.	ъ ю	7	-	A48719	',5'-cvclic-
ო	90	٥.	9	~	150186	',5'-cyclic-
4	1047	29.8	859	7	B34611	3',5'-cvclic-GMP
2	6	6	L)	7	A34810	` `
9	037.	6	5	~	JC4520	',5'-cycli
7.	03	9.	5	~	S13030	',5'-cyclic-
80	02	6	S	Н	A47451	',5'-cyclic-
σ	02	6	S	٦	S06418 .,	',5'-cyclic-
10	02	δ.	S	~	S30762	',5'-cvcli
11	02	6	S	7	A42828	'-cvcli
12	8	8	S	7	A36617	',5'-c <u>v</u> cli
13	97	7.	0	7	S13032 .	,5,
14	933.5	9	7	Н	JC2486	
15	20.	9	2	Н	A40981	,5,
16	79	ά.	g	7	T25590	Vpo
. 17	535.5	ω.	4	Н	S24462	LC)
18	35.	ď.	\leftarrow	7	D88544	R08D7.6
19	381	0	3	7	167945	10
20	365	0	Н	~	S71626 .	in
21	36		^	7	161358	3',5'-cyclic-nucl
22	62.		Н	~	167946	10
23	362.5	。	4	~	I53865	70
24	62.	ö	æ	~	A54442	3',5'-cyclic-nucl
25	362	٥.	æ	7	B53109	.5
26	36	。	7	7	161259	',5'-cycli
27	357.5	ö	S	~	AC2089	deny
28	350	o.	3	Н	A46378	3
29	350	。	3	Н	A44161	, 2,

cyclic nucleotide	cAMP phosphodieste	cyclic-AMP phospho	3',5'-cyclic-AMP p	3',5'-cyclic-nucle	3',5'-cyclic-nucle	phosphodiesterase	3',5'-cyclic-nucle	3',5'-cyclic-nucle	hypothetical prote	3,5'-cyclic-nucle	3',5'-cyclic-nucle	3',5'-cyclic-nucle	3',5'-cyclic-nucle	hypothetical prote	hypothetical prote
T30901	159143	A40949	A47286	JC7266	JC1519	161354	A44162	S55348	T16769	JC6129	T10796	A45334	JW0088	T14783	T24459
7	7	7	7	7	7	7	٦	7	7	٦	7	П	~	7	7
1054	562	564	498	450	564	736	534	. 323	549	536	768	530	713	519	664
6.6	6.6	6.6	6.6	9.8	9.8	8.6	9.7	9.7	9.6	9.6	9.6	9.4	9.4	9.5	9.5
349.5	348	348	347	346	345	345	342.5	339.5	338.5	338	337	331.5	331.5	324.5	322.5
3,															

ALIGNMENTS

C; Genetics: A; Genetics: C; Superfamily: 3', 5'-cyclic-GMP phosphodiesterase 5A; 3', 5'-cyclic-nucleotide phosphorotein; phosphoric diester hy C; Superfamily: 3', 5'-cyclic-nucleotide phosphodiesterase homology <cmpd> C; Superfamily: 3', 5'-cyclic-nucleotide phosphodiesterase homology <cmpd> F; 612-835/Domain: 3', 5'-cyclic-nucleotide phosphodiesterase homology <cmpd> F; 102/Binding site: phosphate (Ser) (covalent) (by CGMP-dependent kinase) #status pre Query Match Best Local Similarity 43.1%; Pred. No. 6.6e-85; Matches 280; Conservative 129; Mismatches 186; Indels 55; Gaps 12; Qy 54 KDRRFNDEIDKLTGYRTKSLLCMPIRSSDGEIIGVAQAIN·KIPEGAPFTEDDEKVMQMY 112 </cmpd></cmpd></cmpd>	RESULT 1 JW0106 3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) 5A - human N:Alternate names: PDE5A1 C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Accession: JW0106 E.Stacey, P.; Rulten, S.; Dapling, A.; Phillips, S.C. Blochem: Blophys. Res. Commun. 247, 249-254, 1998 A.Tille: Molecular cloning and expression of human cGMP-binding cGMP-specific phospho A; Reference number: JW0106; MUID:98308101; PMID:9642111 A; Accession: JW0106 A; Molecule type: mRNA A; Residues: 1.875 <sta> A; Cross.references: GB:AJ004865; NID:93355605; PIDN:CAA06170.1; PID:93355606</sta>
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220

-------DCSDSFSSVFHMECEELEKS--SDTLTREHD 403

367 CTIFIVDE-----

Db

Qγ

221

 $\dot{\Omega}$ Pp δy pp

qq

δý

Qγ

173 CSVLLLEDIESPVVKFTKSFELMSPKCSADAENSFK-----ESMEKSSYSDWL----

LPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCER

113 307

δλ qq

---INNSIAELVASTGLPVNISDAYQDPRFDAEADQISGFH---IRSVLCVPIWN-SNHQ

	625 SICMPLYQALVKNUWKLKPMLDSVATNRSKWEELHOKRILASTASSSS 672 813 AICLQLYEALTHVSEDCFPLLDGCRKNRGKWQALABOOGETLINGESSOT 862 813 AICLQLYEALTHVSEDCFPLLDGCRKNRGKWQALABOOGETLINGESSOT 862 814 III	OY 339 KAEVDKEK
	PRESULT 2 3.5. CYCLIC-CAPP phosphodiasterase (EC 3.1.4.35) 5A - bovine 3.5. CYCLIC-CAPP phosphodiasterase (EC 3.1.4.35) 5A - bovine C. Species: Bos prindganis taurus (cattle) R. Wallister. Lucas, Lucas, Bosine phosphodis (cattle) A. Species: Bosine 265, 12863-2283, 1939 A. Species: Bosine 265, 1947-1499, 1930 A. KDRRPNDEIDKLTGYTKELLONING CORP. Percel Corp. Proceeding Procedure 1947 Bosine 10, 10, 110, 110, 110, 110, 110, 110,	Qy 329 DVLSYHATCSKAEVDKFKAANIPLVSELAIDDIHFDDFSLDVDAMITAALRMFMELG 385

Qy 366 FSLDVDAMITAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLYHNWRHAFNVCQL 425 L ::	810 KALADEYDAKMKVOEEKKÖKOOSAKSAAAGN 58ULT 5 4810 5.5'-cyclic-GMP phosphodiesterase (EC 3.1.4.3 58pecies: Bos primigenius taurus (cattle) Date: 20-Jul-1990 #sequence_revision 20-Jul- Accession: A34810; A34809 Li, T.: Volpp, K.: Applebury, M.L. Title: Bovine cone photoreceptor cGMP phosph Reference number: A34810; MuID:90115860; PMI Accession: A34810 Molecule type: mRNA Residues: 1-855 cLIT. Cross-references: GB:M37838; NID:9163490; PI Charbonneau, H.; Prusti, R.K.; LeTrong, H.; oc. Natl. Acad. Sci. U.S.A. 87, 288-292, 199 CLOSS-references: GB:M37838; NID:9163490; PI Charbonneau, H.; Prusti, R.K.; LeTrong, H.; oc. Natl. Acad. Sci. U.S.A. 87, 288-292, 199 Status: A34809; MuID:90115859; PMI Accession: A34809 Status: preliminary Molecule type: mRNA	A; Residues: 308-502 <cha> A; Residues: 308-502 <cha> A; Cross-references: Gs:M33140; NID:g163492; PIDN:AAA30688.1; PID:g163493; GB:M29465 A; Cross-references: Gs:M33140; NID:g163492; PIDN:AAA30688.1; PID:g163493; GB:M29465 A; Note: parts of this sequence were confirmed by protein sequencing C; Superfamily: 3',5'-cyclic-GWP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotid C; Keywords: cGMP binding; phosphoric diester hydrolase C; Keywords: cGMP binding; phosphoric diesterase homology <cmp> Cuery Match C; Keywords: cGMP binding; phosphoric diesterase homology <cmp> C; Keywords: cGMP binding; diesterase homology <cmp> C; Keywords: cGMP binding; diesterase homology C; Keywords: cGMP binding; diest</cmp></cmp></cmp></cmp></cmp></cmp></cmp></cmp></cmp></cmp></cmp></cmp></cmp></cmp></cmp></cmp></cmp></cha></cha>
Db 464 PTEVESILKYKEKLNVKSIEECDEKDLIRILKEELPDPKDLELYEFRFSDFPVTEHGLIT 523 Oy 376 AALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMYLXHNWRHAFNVCQLMFAMLTTAGF 435 SI:	rase (EC 3.1.4.35) alpha chain - human revision 22-Jun-1990 #text_change 21-Jan-2000 smuth, J.J.; McConnell, D.G.; Champagne, M.S.; ation of human and bovine rod photoreceptor cG ID:9016986; PMID:2155175 P phosphodiesterase alpha chain; 3',5'-cyclic-phoric diester hydrolase nucleotide phosphodiesterase homology <cnp>*: Score 1047; DB 2; Length 859; %: Pred. No. 3.5e-63;</cnp>	DEN

218 174 278 215 338 373	Db 398 DIVGVATFYNRKDGKPFDEHDEYITETLTQFLGWSLLNTDTYDKNKLENRKDIAOEMLM 457 Qy 333 YHATCSKAEVDKF-KAANIPLVSELAIDDIHFDDFSLD 369 1	546
333 PMDHWTLISGLPTYVAENGFICNMLNAPADEYFTFQKGFVDETGWVIKNVLSLPIVNKKE 392 273 QIIGVAQVLNRLDGRPFDDADQRLFEAFVIFCGLGINNTIMYDQVKKSWAKQSVALDVLS 332 1 1 1 1 1 1 1 1 1 1	65 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TESULT 6 17.5cyclic-GMP phosphodiesterase (EC 3.1.4.35) alpha' chain - human C.Species: Homo saplens (man) C.Species: Man, Man, Man, Man, Man, Man, Man, Man,

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3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) alpha chain - bovine
N.Alternate names: cGMP phosphodiesterase alpha chain
C.Speciess Box prindgenius tautus (cattle)
C.Speciess Box prindgenius tautus
C.Speciess Box prindgenius tautus
C.Speciess Box Prindgenius Cattle)
C.Speciess Box Prindgenius Cattle
R.Ovchinnikov, Y.A.; Gubanov, V.V.; Khrantsov, N.V.; Akhmedov, N.B.; Ishchenko, K.A.;
T.M.; Bystrov, N.S.; Severtsova, I.V.; Lipkin, V.M.
Dokl. Biochem. 296, 303-307, 1987
A.Title: Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence of the A; Reference number: S06418
A; Residues: 1-859 cov12
A; Molecule type: mRNA
A; Residues: 1-859 cov12
A; Accession: S27007
A; Residues: 1-859 cov12
A; Accession: S27007
A; Residues: 1-859 cov12
A; Accession: S27007
A; Residues: 2-11; 22-27; 32-40; 95-98; 112-115; 180-193; 248-267; 275-282; 297-306; 312-330; 36
A; Accession: S27007
A; Residues: 2-11; 22-27; 33-40; 95-98; 112-115; 180-193; 248-267; 275-282; 297-306; 312-330; 36
A; Note: this paper is a translation of the Russian paper published in Dokl. Akad. Nau R; Ovchinnikov, Y.A.; Gubanov, V.V.; Khramtsov, N.V.; Ischenko, K.A.; Zagranichny, V.E FEBS Lett. 223, 169-173, 1987
A; Title: Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence of the
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A475.

A475.

A475.

A475.

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A475.

A476.

A476.

Species: Canis lupus familiaris (doy)

C; Species: Or Secope 1999 #text_change 21-Jan-2000

C; Accession: A47451; S14290

R; Suber, M.L.; Pittler, S.J.; Qin, N; Wright, G.C.; Holcombe, V.; Lee, R.H.; Craft, C.M.

A; Title: Irish setter doys affected with rod/cone dysplasia contain a nonsense mutation A; Reference number: A47451; MUID:93248211; PMID:8387203

A; Status: preliminary

A; Accession: A47451

A; Status: preliminary

A; Accession: A47451

A; Status: preliminary

A; Clameral Source: Irish setter, retina

A; Note: sequence inconsistent with the nucleotide translation

A; Note: sequence inconsistent with the nucleotide translation

A; Clameral Source: Irish setter, retina

A; Note: sequence extracted from NCBI backbone (NCBIN:130782, NCBIP:130783)

A; Reference number: 834290

A; Reference number: 834290

A; Residues: 1-184, D', 186-856 CCLE>

A; Cossion: S4230

A; Residues: 1-184, D', 186-856 CCLE>

A; Cossion: Sidio: Sidio: Sidio: Phosphodissterase alpha chain; 3',5'-cyclic-nucleotide phosphodissterase homology CNP>

C; Superfamily: 3',5'-cyclic-nucleotide phosphodissterase homology CNP>
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---MIKOKEFFDVWPVLMGEAPAYSGPRTPDGREINFYKVIDYILHGKEDIK 330
                                                                  VIPNPPADHWALVSGLPPYVAQNGLICNIMNAPAEDFFEFQKEPLDESGWMIKNVLSMPI 390
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                                                                                                                                                                                                                                         HHFNHAVMILQSEGHNIFANLSSKEYSDLMQLLKQSILATDLTLYFERRTEFFELVSKGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----YDWN-----IKNHRDIFRSMLMTACDLGAVTKPWEISRQVAELVTSEFFEQGDRE
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                                          ---KSSYSDWLINNSIAELVASTGLPVNISDAYQDPRFDAEADQI--SGFHIRSVLCVPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              810 KALADEYEAKMKALEEEKOKOOAAKOAASGN 840
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Best Local Similarity
Matches 232; Conserv
SVGLLD--
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photoreceptor cGMP phosphodiesterase al
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A; Residues: 1-2, 'X', 4, 'G', 6-18, 'S', 20-48, 'DV', 51-157, 'T', 159-175, 'C', 177-231, 'R', 233-A; Cross-references: EMBL: X55968; NID: 953616; PIDN: CAA33439.1; PID: 953617
A; Note: the authors translated the codon AG for residue 232 as Glu
C; Superfamily: 3', 5'-cyclic-GMP phosphodiesterase alpha chain; 3', 5'-cyclic-nucleotid
C; Keywords: CGMP binding; phosphoric diester hydrolase
F; 556-789/Domain: 3', 5'-cyclic-nucleotide phosphodiesterase homology <CNP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      441 LENRKDIAQDMVLYHVRCDKDEIQEILPTRDRLGKEPADCEEDELGKILKEELPGPTKFD 500
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                                                                                                                                                                                                                                                                                                                 A. Molecule type: mRNA
A. Residues: 1-856 < CARE>
A. Cross-references: EMBL:X60133; NID:953595; PIDN:CAA42719.1; PID:953596
R. Baehr, W.; Champagne, M.S.; Lee, A.K.; Pittler, S.J.
FEBS Lett. 278, 107-114, 1991
A.71tler: Complete coDNA sequences of mouse rod photoreceptor CGMP phosphodiest cing of the beta-subunit gene.
A. Reference number: S13030; MUID:91130581; PMID:1847109
A. Accession: S13030; MUID:91130581; PMID:1847109
A. Status: preliminary
A. Molecule type: mRNA
A. Residues: 1-559, (6, 561-856 < SBA2>
A. Cross-references: EMBL:X60133
R. Bowes, C.; Li, T.; Danciger, M.; Baxter, L.C.; Applebury, M.L.; Farber, D.E Nature: 347, 677-680, 1990
A. Title: Retinal degeneration in the rd mouse is caused by a defect in the be A. Reference number: S13121; MUID:91013387; PMID:1977087
                                                                      33.752 - 330762 - 330762 - 330762 - 330762 - 34.35) beta chain - mouse 3.5.cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta chain - mouse C;Species: Mus musculus (house mouse) - 5.5 ci. 22-Nov.1993 #sequence_revision 19-Oct-1995 #text_change 21-Jan-2000 C;Accession: S30762; S13031; S13121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EKVMQMYLPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46 LIQRQTKTKDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDD
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Pred. No. 1.1e-61;
                                                                                                                                                                                                                         submitted to the EMBL Data Library, June 1991
A; Reference number: S30762
A; Accession: S30762
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                 A.Accession: S00161
A,Molecule type: mRNA
A;Residues: 1-859 <0.02>
A;Cross-references: EMBL:M27541; NID:g162826; PIDN:AAA30441.1; PID:g162828
A;Note: part of this sequence was confirmed by protein sequencing
A,Note: part of this sequence was confirmed by protein sequencing
A,Note: 381-741 was also found
R;Pittler, S.J.; Baehr, W; Wasmuth, J.J.; McConnell, D.G.; Champagne, M.S.; vanTuinen,
Genomics 6, 272-283, 1990
A;Titler: Molecular characterization of human and bovine rod photoreceptor cGMP phosphodi
A;Title: Molecular characterization of human and bovine rod ophotoreceptor cGMP phosphodi
A;Reference number: A34611; MUID:90169986; PMID:2155175
A;Recession: A34611
A;Molecula type: mRNA
A;Residues: 1-193, VV, 195-423, TY, 425-674, FF, 676-859 <PIT>
A;Residues: 1-193, VV, 195-423, TY, 425-674, FF, 676-859 <PIT>
A;Cross-references: GB:M26443; NID:g162833; PIDN:AAA30443.1; PID:g162834
C;Comment: This protein is involved in the transduction and amplification of the visual C;Superfamily: 3, 5, cyclic-GMP phosphodiesterase alpha chain: 3',5'-cyclic-nucleotide F;2-859/Product: 3',5'-cyclic-GMP phosphodiesterase alpha chain #status experimental cMR F;558-791/Domain: 3',5'-cyclic-mucleotide phosphodiesterase homology cCNP>
F;2/Modified site: acetylated amino end (Gly) (in mature form) #status experimental
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S00161; MUID:88030033; PMID:2822478
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Db 561 HGFNVAQTMFTLLMTGKLKSYYTDLEAFAMVTAGLCHDIDHRGTNNLYQMKSQNPLAKLH 620 Qy 478 GTSATLEHHHFNHAVMILQSEGHNIFANLSKEVSDLMQLLKOSILATDLTLYFERRTEF 537 1 1 1 1 1 1 1 1 1 1	RESULT 11 A42828 3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta chain - human c;Species: Homo saptens (man) C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000 C;Accession: A42828; S34590; S18715 R;Collins, C.: Hutchinson, G.; Kowbel, D.; Riess, O.; Weber, B.; Hayden, M.R. Genomics 13, 698-704, 1992 A;Title: The human beta-subunit of rod photoreceptor cGMP phosphodiesterase: complete re A;Reference number: A42828; MUID:92347868; PMID:1322354 A;Reference number: A42828 A;Reference number: A42828 A;Residues: 1-684 <col.> A;Residues: 1-684 <col.> A;Residues: 1-684 <col.> A;Coss-references: GB:S41458; NID:9252252; PIDN:AAB22690.1; PID:q252253 A;Note: sequence extracted from NCB1 backbone (NCBIR:109783, NCBIP:109784) R;Khramtsov, N.V.; Feshchenko, E.A.; Suslova, V.A.; Shmukler, B.E.; Terpugov, B.E.; Raki FEBS Lett. 327, 275-278, 1993 A;Title: The human rod photoreceptor cGMP phosphodiesterase beta-subunit. Structural stu A;Reference number: S34590; MUID:93351644; PMID:8394243 A;Status: preliminary A;Status: preliminary</col.></col.></col.>	Andrew, S.; Sc ding the beta-	Query Match 29.0%; Score 1020; DB 2; Length 854; Best Local Similarity 34.4%; Pred. No. 2.4e-61; Matches 229; Conservative 118; Mismatches 240; Indels 78; Gaps 11; Qy 58 FNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMOMYLPFCG 117

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                                                   R.Ovchinnikov, Y. A.; Gubanov, V. V.; Khramtsov, N. V.; Ischenko, K. A.; Zagranichny, V. E.; FEBS Lett. 223, 169-173, 1987

A.Title: Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence of the alp A. Reference number: S00161; MUID:88030033; PMID:282478

A. Reference number: S00161; MUID:88030033; PMID:282478

A. Status: nucleic acid sequence not shown

A. Status: ad-536, TRRSWC', 542-596, TY', 598-601, WV', 603-606, 'OLI' < OVC)

C. Superfamily: 3', 5' -cyclic-GMP phosphodiesterase alpha chain; 3', 5' -cyclic-nucleotide phosphodiesterase beac chain #status predicted < WAT>

F; 556-789/Domain: 3', 5' -cyclic-nucleotide phosphodiesterase homology < CNP>

F; 2. Modified site: acetylated amino end (Ser) (in mature form) #status experimental
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Residues: 1-2,'P',4-90,'P',92-93,'H',95-202,'VN',205-489,491-853 <LI2>
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S13032
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta'
C:Species: Mus musculus (house mouse)
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Best Local Similarity
Matches 230; Conserv
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A;Cross-references: GB:X87952; EMBL:X60133; NID:9871432; PIDN:CAA61202.1; PID:9871433 CS:Superfamily: 3',5'-cyclic-GMP phosphoiesterase alpha chain; 3',5'-cyclic-nucleotid C;Keywords: alternative splicing; cGMP binding; bhosphoric diester hydrolase F;556-790/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
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C; Date: 21;Nov-1993 #sequence_revision 10-Nov-1995 #text_ch C; Accession: S13032; S30763
R; Baehr, W.; Champagne, M.S; Lee, A.K.; Pittler, S.J.
FEBS Lett. 278, 107-114, 1991
A; Title: Complete CDNA sequences of mouse rod photoreceptor cing of the beta-subunit gene.
A; Reference number: S13030; MUID:91130581; PMID:1847109
A; Accession: S1303
A; Molecule type: DNA
A; Residues: 1-800 cBAE>
A; Cross-references: EMBL:X60133
R; Baehr, W.
Submitted to the EMBL Data Library, June 1991
A; Reference number: S30762
A; Accession: S30763
A; Accession: S30763
A; Molecule type: DNA
A; Residues: 1-559, W. V. 561-800 cBAE>
A; Molecule type: DNA
A; Residues: 1-559, W. V. 561-800 cBAE>
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3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cGMP-stimulated - rat
N'Alternate names: cGMP-dependent phosphodiesterase
C;Species: Rattus norvegicus (Norway rat)
C;Bate: 26-Aug-1999 #sequence_revision 26-Aug-1999 #text_change 05-Nov-1999
C;Accession: JC2486
R;Yang, O: Paskind, M.; Bolger, G.; Thompson, W.J.; Repaske, D.R.; Cutler, L.S.; Epstei
Biochem. Biophys. Res. Commun. 205, 1850-1858, 199;
R;Yang, O: Paskind, M.; Bolger, G.; Thompson, W.J.; Repaske, D.R.; Cutler, L.S.; Epstei
Biochem. Biophys. Res. Commun. 205, 1850-1858, 199;
A;Reference number: JC2486; MUID:95110334; PMID:7811274
A;Recence number: JC2486
A;Molecule type: mRNA
A;Residues: 1-928 etAnA
A;Residues: 1-928 etAnA
A;Residues: 1-928 etAnA
A;Cross-references: GB:U1101; NID:9706929; PIDN:AAA63683.1; PID:9706930
A;Experimental source: brain
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase, CGMP-stimulated; 3',5'-cyclic-C;Reywords: alternative splicing; cAMP binding; homodimer: phosphoprotein;
F;643-865/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology cCNPD>
F;109/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A40981
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cGMP-stimulated - bovine
N;Alternate names: cGMP-dependent phosphodiesterase
C;Species: Bos primigenius taurus (cattle)
                                                                                                                                                                                                                                                                                                                                                                                                                       12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RGTNNAFQAKSGSALAQLYGT-SATLEHHHFNHAVMILQSEGHNIFANLSSKEYSDLMQL 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OMYLPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLK 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QHCFHYTGTVLTSTLAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLLQEIITEARNLSN 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CERCSVLLLEDIESPVVKF----TKSFELMSPKCSADAENSFKESMEKSSYSDWLINN 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIAELVASTGLPVNISDAYQDPRFDAEADQISGFHIRSVLCVPIWNSNHQIIGVAQVLNR 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LDGKPFDDADQRLFEAFVIFCGLGINNTIMYDQVKKSWAKQSVALDVLSYHATCSKAEVD 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KFKAANIPLVSELAIDDIHFDDF----SLDVDAMITAALRMFMELGWQKFKIDYETLC 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLLHDGIQPVAAI --- DSNFANFTYTPRSLPEDDTSMAILSMLQDMNFINNYKIDCPTLA 628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RQVAELVISEFFEQGDRERLELKLIPSAIFDRNRKDELPRLQLEWIDSICMPLYQALVKV 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTRNILCFPIKNENQEVIGVAELVNK
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       47;
                                                                                                                                                                                                                                                                                                                                                                           26.6%; Score 933.5; DB 1; Length 928; larity 33.2%; Pred. No. 2.1e-55; Conservative 131; Mismatches 246; Indels 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NVKLKPMLDSVATNRSKWEELHQKRLLASTASSSS 672
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AEICSVFLLDQNELVAKVFDGGVVDDESYEIRIP-
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Matches 211;
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R;Charbonneau, H.; Beier, N.; Walsh, K.A.; Beavo, J.A. Proc. Natl. Acad. Sci. U.S.A. 83, 9308-9312, 1986
A;Title: Identification of a conserved domain among cyclic nucleotide phosphodiestera
A;Reference number: A26650; MUID:87092242; PMID:3025833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RiTahaka, T.; Hockman, S.; Moos Jr., M.; Taira, M.; Meacci, E.; Murashima, S.; Mangan Second Messengers Phosphoproteins 13, 87-98, 1991
A:Title: Comparison of putative cGMP-binding regions in bovine brain and cardiac cGMP A; Reference number: A60179; MUID:95056414, PMID:1659635
C;Date: 26-Aug-1999 #sequence_revision 26-Aug-1999 #text_change 05-Nov-1999 C;Accession: A40981; B36112; A36112; B26650; A60179; C26650 R;Sonnenburg, W.K.; Mullaney, P.J.; Beavo, J.A. Biol. Chem. 266, 17655-17661, 1991 A;Title: Molecular cloning of a cyclic GMP-stimulated cyclic nucleotide phosphodieste A;Reference number: A40981; MUID:91373395; PMID:1654333 A;Accession: A40981.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Amino acid sequence of the cyclic GMP stimulated cyclic nucleotide phosphodi
A;Reference number: A36112; MUID:91104948; PMID:2176866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.Molecule Type: mRNA
A.Residues: 311-803, DV, 806-921 (TAN)
A.Residues: 311-803, DV, 806-921 (TAN)
A.Residues: part of this sequence was confirmed by protein sequencing
C.Comment: This protein is not glycosylated.
C.Superfamily: 3', 5'-cyclic-nucleotide phosphodiesterase, cGMP-stimulated: 3',5'-cycl
C.Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase homology cGNPD>
F:1/Modified site: acetylated amino end (Met) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                              Beavo,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DDEKVMÖMYLPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHR 163
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                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-921 <SON>
A;Cross-references: GB:M73512; NID:g162829; PIDN:AAA74559.1; PID:g162830
                                                                                                                                                                                                                                                                                                                                                                                                              Sonnenburg, W.K.; Stroop, S.D.; Walsh, K.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: not compared with conceptual translation
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A;Residues: 1-203,'D',205-477,'Q',479-921 <LET2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein
A; Residues: 613-632, 'L', 634-794;808-868 <CHA>
A; Experimental source: heart
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                                                                                                                                                                                                                                                                                                                                                                                                              Trong, H.; Beier, N.; Sonnenbu
temistry 29, 10280-10288, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 592-921 <LET>
A;Accession: A36112
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Search completed: June 13, 2003, 15:49:42 Job time: 44.4875 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 13, 2003, 15:38:49; Search time 14.0228 Seconds (without alignments) 2023.123 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-663-542-1 3516 1 MLKQARRPLFRNVLSATQWK......ASTASSSSPASVMVAKEDRN 684

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 segs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	. 076074 homo sapien	canis f	Q28156 bos taurus	rattus	gallus	homo sa	bos tau	pos	P27664 muscmusculu	hom	canis	P35913 homo sapien	mus m	can	P23439 bos taurus	homo		rattu		cae	Q922s4 mus musculu				076083 homo sapien	54	5	S)	74	P27815 homo sapien	ratt	Q9qxq1 mus musculu 001065 mus musculu	2
SUMMARIES	TD	CN5A_HUMAN	CN5A_CANFA	CN5A_BOVIN	CN5A_RAT	CNRC_CHICK	CNRA_HUMAN	CNRC_BOVIN	CNRA_BOVIN	CNRA_MOUSE	CNRC_HUMAN	CNRB_CANFA	CNRB_HUMAN	CNRB_MOUSE	CNRA_CANFA	CNRB_BOVIN	CN10_HUMAN	CN2A_HUMAN	CN2A_RAT	CN2A_BOVIN	YB2J_CAEEL	CN2A_MOUSE	YNE6_CAEEL	REGA_DICDI	CN9A_MOUSE	CN9A_HUMAN	CN4C_RAT	CN4C_HUMAN	CN4D_HUMAN	CN4A_RAT	CN4A_HUMAN	CN4D_RAT	CN7B_MOUSE	1 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2 -
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ALIGNMENTS

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                                                        ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: EXPRESSED IN AORTIC SMOOTH MUSCLE CELLS,
HEART, PLACENTA, SKELETAL MUSCLE AND PANCREAS AND, TO A MUCH
LESSER EXTENT, IN BRAIN, LIVER AND LUNG.
DOMAIN: COMPOSED OF A C-TERMINAL CATALYTIC DOMAIN COMPOSED OF A C-TERMINAL CATALYTIC DOMAIN CONTAINED THO BUTATIVE DIVALENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN
WHICH CONTAINS TWO HOMOLOGOUS ALLOSTERIC CGMP-BINDING REGIONS, A
        POTENT INHIBITOR OF PDESA AND IS EFFECTIVE IN THE TREATMENT OF PENILE ERECTILE DYSFUNCTION, ALSO INHIBITED BY ZAPRINAST. PATHWAY: CYCLIC nucleotide metabolism.

ALTERNATIVE PRODUCTS: 2 ISOFORMS; PDE5Al (SHOWN HERE) AND PDE5A2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00126; PDEASE_1; 1.
Hydrolase; cGMP; cGMP-binding; Phosphorylation; Alternative splicing;
Zinc; Repeat.
 REGULATION: SILDENAFIL (VIAGRA) IS A HIGHLY SELECTIVE AND
                                                                                                                                                           PTM: PHOSPHORYLATION IS REGULATED BY BINDING OF CGMP TO THE TWO ALLOSTERIC SITES (BY SIMILARITY).
SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
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CGMP (BY SIMILARITY).
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InterPro; 1PR003607; ME_Pplase_HDc.
InterPro; 1PR002073; PDEase.
Dfan: PF0023; PDEase: 1.
Pfam: PF01590; GAF; 2.
PRINTS; PR0387; PDIESTERASE1.
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BAA33372.1;
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SMART; SM00471; HDC; 1.
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AB015656;
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                                                                                                                                                                                                                                                                                                         ---INNSIAELVASTGLPVNISDAYQDPRFDAEADQISGFH---IRSVLCVPIWN-SNHQ 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           274 IIGVAQVLNRLDG-----KPFDDADQRLFEAFVIFCGLGINNTIMYDQVKKSWAKQSVAL 328
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            ZINC 1 (POTENTIAL).
ZINC 1 (POTENTIAL).
ZINC 1 (POTENTIAL).
ZINC 2 (POTENTIAL).
MERAGPSFGQORQQQQQQQQQDQSVEAWLDDHWDFT
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                                                                                                                                                                                                                                                                 247 EDPRFNAEVDQITGYKTQSILCMPIKNHREEVVGVAQAINKKSGNGGTFTEKDEKDFAAY
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O77746; O77747;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
CGMP-specific 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (CGB-PDE)
(CGMP-binding CGMP-specific phosphodiesterase).
CGBI-DESA OR PDE5.
Canis familiaris (Dog).
                                                                                                             FSYFVRKA -> MLPFGDK (IN ISOFORM PDE5A2)
MISSING (IN REF. 2; BAA33372).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              625 SICMPLYQALVKVNVKLKPMLDSVATNRSKWEEL - - HQKRLLASTASSSS 672
                                                                                                                                                                                DB 1; Length 875;
                                                                                                                                                                             Query Match 38.9%; Score 1366.5; DB 1; Length Best Local Similarity 43.1%; Pred. No. 1.3e-83; Matches 280; Conservative 129; Mismatches 186; Indels
 PHOSPHORYLATION (POTENTIAL)
                                                                                                                                        -> G (IN REF. 4).
91EA8C33B6CD254D CRC64;
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102
613
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682
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CONFLICT
SEQUENCE
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VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: BOTH ISOFORMS BYRRESSED ABUNDANTLY IN THE
CEREBELLUM, HIPPOCAANDES, RETINA, LUNG, HEART, SPLERN, AND THORACIC
ARTERY. PDESAI, BUT NOT PDE5A2, IS ALSO ABUNDANTLY EXPRESSED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN: COMPOSED OF A C-TERMINAL CATALYTIC DOMAIN CONTAINING TWO PUTATIVE DIVALENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN WHICH CONTAINS TWO HOMOLOGOUS ALLOSTERIC GGMP-BINDING REGIONS, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00126; PDEASE_I; 1.
Hydrolase; cGMP; cGMP-binding; Phosphorylation; Alternative splicing;
                                                                                                                                                                                                                                        ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALTERNATIVE PRODUCTS: 2 ISOFORMS; PDE5A1 (SHOWN HERE) AND PDE5A2;
                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)0 = guanosine 5'-phosphate.
GUAROTOR: REQUIRES DIVALENT CATIONS. ZINC IONS ARE REQUIRED FOR MAXIMUM ACTIVITY. MANGANESE, MAGNESIUM AND COBALT ALSO SUPPORT CATALYSIS BUT AT MUCH HIGHER CONCENTRATIONS (BY SIMILARITY).
ENZYME REGULATION: INHIBITED BY ZAPRINAST.
SURGELLULAR LOCATION: TOPESA1 AND POESA2 ARE LOCATED MOSTLY TO SUBCELLULAR LOCATIONS AND SOME TO PARTICULAR ELLULAR.
                                                                                                                                                                           Biol. Chem. 273:26982-26990(1998).
- FUNCTION: PLAYS A ROLE IN SIGNAL TRANSDUCTION BY REGULATING THE INTRACELLULAR CONCENTRATION OF CYCLIC NUCLEOTIDES. THIS PHOSPHODIESTERASE CATALYZES THE SPECIFIC HYDROLYSIS OF CGMP TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION IS REGULATED BY BINDING OF CGMP TO THE TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALLOSTERIC SITES (BY SIMILARITY).

MISCELLANEOUS: CGMP-BINDING TO THE ALLOSTERIC SITES IS STIMULAT
BY 3-ISOBUTYL-1 METHYLXANTHINE (IBMX).
SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
FAMILY.
   Euteleostomi;
                                                                                                                         Kotera J., Fujishige K., Akatsuka H., Imai Y., Yanaka N., Omori P
"Novel alternative splice variants of cGMP-binding cGMP-specific
phosphodiesterase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGMP (BY SIMILARITY).
CATALYTIC (BY SIMILARITY).
ZINC 1 (POTENTIAL).
ZINC 1 (POTENTIAL).
                 Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                      SEQUENCE FROM N.A. (ISOFORMS PDE5A1 AND PDE5A2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003607; ME_Pplase_HDc.
InterPro; IPR002073; PDEase.
                                                                                                          MEDLINE=98434620; PubMed=9756948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS: PR00387; PDIESTERASE1.
SMART; SM00065; GAF; 2.
SMART; SM00471; HDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB008467; BAA33503.1; -. EMBL; AB008468; BAA33504.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00233; PDEase; 1
Pfam; PF01590; GAF; 2.
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500
276
277
289
478
843
92
603
                 Mammalia; Euther
NCBI_TaxID=9615;
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                                                                                         TISSUE=Lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zinc; Repea
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                                                                                                                                                                                                       276 GVAQVLNRLDG-----KPFDDADQRLFEAFVIFCGLGINNTIMYDQVKKSWAKQSVALDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CSVLLLEDIESPVVKFTKSFELMSPKCSADAENSFK-----ESMEKSSYSDWL-----
                                                                                                                                                                                                                                                                 ------DCSDSFSSVFHMECEELEKLPDTLTRERDAN
                                                                                                                                                                                                                                                                                           -INNSIAELVASTGLPVNISDAYQDPRF----DAEADQISGFHIRSVLCVPIWN-SNHQII
                                                                                                                                                                                                                                                                                                                 396 RINYMYAQYVKNTMEPLNIPDVSKDKRFPWTNENTGNVNQQCIRSLLCTPIKNGKKNKVI
                                                                                                                                                                                                                                                                                                                                                       LSYHATCSKAEVDKFK---AANIPLVSELAIDDIHFDDFSLDVDAMITAALRMFMELGMV
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EDPRFNAEVDQITGYKTQSILCMPIKNHREEVVGVAQAINKKSGNGGTFTEKDEKDFAAY
                                                                                                                                                                                            LPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCER
                                                                                                                                                                                                                                                                                                                                                                                                                                        QKFKIDYETLCRWLLTVRKNYRM-VLYHNWRHAFNVCQLMFAMLTTAGFQDILTEVEILA
                                             MERGSPGÄGAARLPRDQÖSVEAMLDDHRDFTFSYFVKKAT
-> MLPFGHQR (IN ISOFORM PDE5A2).
F20BB37B71E93BB6 CRC64;
                                                                                                                                             KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAIN~KIPEGAPFTEDDEKVMQMY
                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
cGMP-specific 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (CGB-PDE)
PDE5A OR PDE5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                    51;
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                                                                                             Length
                                                                                                                     Mismatches 190; Indels
ZINC 1 (POTENTIAL).
ZINC 2 (POTENTIAL).
ZINC 2 (POTENTIAL).
ZINC 2 (POTENTIAL).
                                                                                            Score 1357.5; DB Pred. No. 5.3e-83;
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                                                                                                                     Conservative 129;
                                                                      98293 MW;
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Bovidae; Bovinae; Bos
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Les 278; Conserv
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Q28156;
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                                                VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Identification of key amino acids in a conserved {\tt cGMP-binding} site of {\tt cGMP-binding} phosphodiesterases. A putative NKXnD motif for {\tt cGMP}
                                                                                                                                                                                                                                                                                                                                                                                                                          Turko I.V., Haik T.L., McAllister-Lucas L.M., Burns F., Francis S.H., Francis S.H., Corbin J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN: COMPOSED OF A C-TERMINAL CATALYTIC DOMAIN CONTAINING TWO PUTATIVE DIVALENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WHICH CONTAINS TWO HOMOLOGOUS ALLOSTERIC CGMP-BINDING REGIONS, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Finchem. J. 329;505-510(1998)...
-!- FOUCTION: PLAYS A ROLE IN SIGNAL TRANSDUCTION BY REGULATING THE INTRACELLUIAR CONCENTRATION OF CYCLIC NUCLEOTIDES. THIS PHOSPHODIESTERASE CATALYZES THE SPECIFIC HYDROLYSIS OF CGMP TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION IS REGULATED BY BINDING OF CGMP TO THE TWO
                                                                                                                                                                                                                                                                              MEDLINE=99107229; PubMed=8530505; McAllister-Lucas L.M., Haik T.L., Colbran J.L., Sonnenburg W.K., Seger D., Turko I.V., Beavo J.A., Francis S.H., Corbin J.D.; An essential aspartic acid at each of two allosteric cGMP-binding sites of a cGMP-specific phosphodiesterase."; J. Biol. Chem. 270:30671-30679(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALLOSTERIC SITES.
SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COFACTOR: REQUIRES DIVALENT CATIONS. ZINC IONS ARE REQUIRED FOI MAXIMOM ACTIVITY. MANGAMES, MASENESHMA AND COBALT ALSO SUPPORT CATALYSIS BUT AT MUCH HIGHER CONCENTRATIONS.

ENZYME REGULATION: MOST POTENTLY INHIBITED BY ZAPRINAST AND
                                                                                                                                                                                     Francis S.H., Colbran J.L., McAllister-Lucas L.M., Corbin J.D.;
"Zinc interactions and conserved motifs of the CGMP-binding cGMP-
specific phosphodiesterase suggest that it is a zinc hydrolase.";
J. Biol. Chem. 269:22477-22480(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cGMP-binding cGMP-
                                                                                          cGMP-specific
                                          McAllister-Lucas L.M., Sonnenburg W.K., Kadlecek A., Seger
Trong H.L., Colbran J.L., Thomas M.K., Walsh K.A., Francis
Corbin J.D., Beavo J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phosphodiesterase (PDE5) is required for its
                                                                                       "The structure of a bovine lung cGMP-binding, ophosphodiesterase deduced from a cDNA clone."; J. Biol. Chem. 268:22863-22873(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION, AND MUTAGENESIS.
MEDILE-98109724; PUDMed-946376;
TURKO I.V., Francis S.H., Corbin J.D.;
"Binding of cGMP to both allosteric sites of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIPYRIDAMOLE.
PATHWAY: Cyclic nucleotide metabolism.
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biol. Chem. 271:22240-22244(1996).
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InterPro; IPR003607; ME_Pplase_HDc.
                                                                                                                                                       METAL-BINDING.
MEDLINE=94357882; PubMed=8077192;
                            MEDLINE=94043054; PubMed=8226796;
                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96355629; PubMed=8703039;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 KDRRENDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAIN-KIPEGAPFTEDDEKVMQMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K->A: DECREASED CGMP-BINDING; NO CHANGE IN CATALYTIC ACTIVITY.

K->R: SLIGHT INCREASE IN CGMP-BINDING.
D->A: DECREASED CGMP-BINDING; NO CHANGE IN CATALYTIC ACTIVITY.
D->N: INCREASED CGMP-BINDING; NO CHANGE
                                                                                                                                                                                                                                                                                                                                                                NO CHANGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHANGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E->A: NO CHANGE IN CGMP-BINDING.
D->A: INCREASED CGMP-BINDING; NO CHANG
IN CATALYTIC ACTIVITY...PHOSPHORYLATED
LOWER CONCENTRATIONS OF CGMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 865;
                                                                                                                                                                                                                                                                                                                                                (TIC (BY SIMILARITY).
DECREASED CGMP-BINDING;
                                                                                                                ; Phosphorylation; Zinc; Re
PHOSPHORYLATION (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2FF7144B2990B4F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                               IN CATALYTIC ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IN CATALYTIC ACTIVITY.
                                                                                                                                             ZINC 1 (POTENTIAL).
ZINC 1 (POTENTIAL).
ZINC 1 (POTENTIAL).
ZINC 2 (POTENTIAL).
ZINC 2 (POTENTIAL).
ZINC 2 (POTENTIAL).
GGMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38.6%; Score 1355.5; DB 42.9%; Pred. No. 7.2e-83; tive 129; Mismatches 18
                                                                                                                                                                                                                                                              CGMP.
                                                                                                                                                                                                                                                                                                 CGMP.
                                                                                                                                                                                                                                                                                                                CGMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             larity 42.9%; Pr. Conservative 129;
                                                                                                               cGMP-binding;
                                                                                               PROSITE; PS00126; PDEASE_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98626 MW;
                                              PRINTS, PR00387; PDIESTERASE1
SMART; SM00065; GAF; 2.
SMART; SM00471; HDC; 1.
IPR002073; PDEase.
             Pfam; PF00233; PDEase; 1.
Pfam; PF01590; GAF; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            290
                                                                                                                                                                                                                                                                                                                                                                                                                             277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 279; Conserv
                                                                                                                  CGMP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 865
                                                                                                                Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                METAL
NP_BIND
NP_BIND
                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                              MOD_RES
                                                                                                                                                                                                                                                                                                                BINDING
                                                                                                                                                                                                                                                                                                                                 BINDING
                                                                                                                                                                                                                                                                                                                                                                                                MUTAGEN
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505 NLSSKEYSDLMOLLKOSILATDLTLYFERRTEFFELVSKGEYDWNIKNHRDIFRSMLMTA 564
                 CDLGAVTKPWEISRQVAELVTSEFFEQGDRERLELKLTPSAIFDRNRKDELPRLQLEWID
                                                                              STRAIN=Sprague-Dawley, TISSUE-Lung,
MEDLINE=98036118; PubMed=9370351;
Kotera J., Yanaka N., Fujishige K., Imai Y., Akatsuka H., Ishizuka T.,
Kawashima K., Omori K.; Julishige K., Imai Y., Akatsuka H., Ishizuka T.,
Expression of rat cGMP-binding cGMP-specific phosphodiesterase mRNA
in Purkinje cell layers during postnatal neuronal development.";
Eur. J. Biochem. 249:434-442[1997].
Fur. J. Biochem. 249:434-442[1997].
INTRACELLULAR A ROLE IN SIGNAL TRANSDUCTION BY REGULATING THE
INTRACELLULAR CONCENTRATION OF CYCLIC NUCLEOTIDES. THIS
PHOSPHODIESTERASE CATALXZES THE SPECIFIC HYDROLXSIS OF CGMP TO 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PATHWAY: CYCLIC nucleotide metabolism.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; PDE5A1 AND PDE5A2 (SHOWN HERE);
ARE PRODUCED BY ALTERNATIVE SPLICING.
DOMAIN: COMPOSED: OF A C-TERMINAL CATALYTIC DOMAIN CONTAINING TWO
PUTATIVE DIVALENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN
WHICH CONTAINS TWO HOMOLOGOUS ALLOSTERIC CGMP-BINDING REGIONS, A
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae, Rattus
                                                                                                                                                                                                                                                         15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
cGMP-specific 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (CGB-PDE)
PDE5A OR PDE5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: PHOSPHORYLATION IS REGULATED BY BINDING OF CGMP TO THE TWO ALLOSTERIC SITES (BY SIMILARITY).
SIMILARITY: BELONGS TO THE CYCLIC 'NUCLEOTIDE PHOSPHODIESTERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            guanosine 5'-phosphate.
COFACTOR: REQUIRES DIVALENT CATIONS. ZINC IONS ARE REQUIRED FOR MAXIMUM ACTIVITY. MANGANESE, MAGNESIUM AND COBALT ALSO SUPPORT CATALYSIS BUT AT MUCH HIGHER CONCENTRATIONS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)0
                                                                                                                     833 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003018; GAF.
InterPro; IPR003607; ME_Pplase_HDc.
InterPro; IPR002073; PDEase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00233; PDEase; 1.
Pfam; PF01590; GAF; 2.
PRINTS; PR00387; PDESTERASE1.
SMART; SM00065; GAF; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D89093; BAA23672.1; -.
                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND B.
                                                                                                                                                                                                                             CN5A_RAT
054735;
                                                                                                                       625
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CN5A_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---KPFDDADQRLFEAFVIFCGLGINNTIMYDQVKKSWAKQSVALDVLSYHATCSKAEVD 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               520 QSILATDLTLYFERRTEFFELVSKGEYDWNIKNHRDIFRSMLMTACDLGAVTKPWEISRQ 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               580 VAELVTSEFFEQGDRERLELKLTPSAIFDRNRKDELPRLQLEWIDSICMPLYQALVKVNV 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | | ||:: :| ||||| :|:|||||: |::|| |: ||:|| |:::|
617 GVNNSYIQRSEHPLAQLY-CHSTMEHHFPDQCLMVLNSPGNQILSGLSIEEYKTTLKIIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 CSVLLLEDIESPVVKFTKSFELMSPKCSADAENSFKESMEKSSYSDWLINNSIAELVAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 GLPVNISDAYQDPRF---DAEADQISGFHIRSVLCVPIWN-SNHQIIGVAQVLNRLDG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLTVRKNYRM-VLYHNWRHAFNVCQLMFAMLTTAGFQDILTEVEILAVIVGCLCHDLDHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   460 GTNNAFQAKSGSALAQLYGTSATLEHHHFNHAVMILQSEGHNIFANLSSKEYSDLMQLLK
                                                                                                                                                                                                                                                                                                                                                                             KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGE1IGVAQAIN-KIPEGAPFTEDDEKVMQMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KFK---AANIPLVSELAIDDIHFDDFSLDVDAMITAALRMFMELGMVQKFKIDYETLCRW
                PROSITE; PS00126; PDEASE_I; 1.
Hydrolase; cGMP; cGMP-binding; Phosphorylation; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                              26;
                                                                                                                                                                                                                                                                                                            Length 833;
                                                          CGMP (BY SIMILARITY).
CATALYTIC (BY SIMILARITY).
PHOSPHORYLATION (POTENTIAL).
ZINC 1 (POTENTIAL).
ZINC 1 (POTENTIAL).
ZINC 2 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                            Pred. No. 1.2e-82;
9; Mismatches 198;
                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                  Score 1352; DB 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      862
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                             Conservative 129;
                                                                                                                                                                                                                                                                                  94556 MW;
                                                                                                                                                                                                                                                                                                              38.5%;
43.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                    571
575
600
611
615
640
SMART; SM00471; HDc; 1
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 275; Conserv
                                                                                                                                                                                                                                                                                833 AA;
                                                            1196
378
2244
2244
2257
446
546
60
571
600
                                                inc; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNRC_CHICK
P52731;
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                                                                                                                                                                                                                                                                                  SEQUENCE
                                                            NP_BIND
NP_BIND
BINDING
BINDING
BINDING
BINDING
DOMAIN
                                                                                                                                                                       MOD_RES
METAL
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CNRC_CHICK
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METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 TRLLNVTPTS-----KFEDNLVNPDKETVFPLDIGIAGWVAHTKKFFNIPDVKKNNHFS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEIDKITGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYLPFCGIA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 ISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCERCSVLLL- 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INNSIAELVASTGLPVNISDAYQDPRFDAEADQI--SGFHIRSVLCVPIWNSNHQIIGVA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KDRRFN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----EDIESPVVKFTKSFELMSPKCSADAENSF------KESME---KSSYSDWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         284 MTKEKEFYDEWPIRLGEAEPYKGPKTPDGREVNFYKIIDYILHGKEEIKVIPTPPADHWC
                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                    guanosine 5'-phosphate.
SUBUNITS THAT ARE ASSOCIATED
SUBUNITS THAT ARE ASSOCIATED
WITH 3 SMALLER PROTEINS OF 11, 13, AND 15 kDa.
SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
                                                                                                                                                                                                                                                           MEDLINE-95121406; PubMed-7821382; Semple-Rowland S.L., Green D.A.; Semple-Rowland S.L., Green D.A.; Molecular characterization of the alpha'-subunit of cone photoreceptor cGMP phosphodiesterase in normal and rd chicken."; Exp. Eye Res. 59:365-372(1994).
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Cone cGMP-specific 3',5'-cyclic phosphodiesterase alpha'-subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00126; PDEASE_I; 1.
Hydrolase; cGMP; Vision; Prenylation; Lipoprotein; Membrane.
LIPID 859 859 GERANYL.GERANYL (BY SIMILARITY).
SEQUENCE 862 Aa; 100008 MW; BD3145BB5FF826A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 TRLVQISGASLAEKQEKHQDFLIQRQTKT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.1%; Score 1060; DB 1; 32.8%; Pred. No. 3.7e-63; iive 139; Mismatches 251;
                                                                                                                                                                                                                                              STRAIN=Rhode Island red; TISSUE=Retina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro, IPR003018; GAF.
InterPro, IPR003607; ME_Pplase_HDc.
InterPro, IPR002073; PDEase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001230; Prenyl_site.
Pfam; PF00233; PDEase; 1.
Pfam; PF01590; GAF; 2.
SMART; SM00065; GAF; 2.
SMART; SM00065; GAF; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative 139;
                                                                                                              Gallus gallus (Chicken).
Rukarvota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L29233; AAC42223.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                           NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                             FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233;
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279 QVLNRLDGKPFDDADQRLFEAFVIFCGLGINNTIMYDQVKKSWAKQSVALDVLSYHATCS 338
                                                                      375
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                                                                                                                                           376 AALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLYHNWRHAFNVCQLMFAMLTTAGF 435
                                                                                                                                                                                                                 QDILTEVEILAVIVGCLCHDLDHRGTNNAFQAKSGSALAQLYGTSATLEHHFNHAVMIL 495
                                                                                                                                                                                                                                                                                                                                                                                 104 TFYNRKDGKPFDEYDEQIIETLTQFLGWSVLNTDTYDKMNKLENRKDIAQEMLMYQTKAT
                                                                                             ||: |:| : | | | 464 PTEVESILKYKEKLNVKSIEECDEKDLIRILKEELPDPKDLELYEFRFSDFPVTEHGLIT
                                                                                                                                                                                                                                                                                                                                                            YDWNIKNHRDIFRSMLMTACDLGAVTKPWEISRQVAELVTSEFFEQGDRERLELKLTPSA
                                                                        -----AANIPLVSELAIDDIHFDDFSLDVDAMIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Autosomal recessive retinitis pigmentosa caused by mutations in the alpha subunit of rod cGMP phosphodiesterase.";

Nat. Genet. 11:468-471(1995).

Nat. Genet. 11:468-471(1995).

AND AMPLIFICATION OF THE VISUAL. SIGNAL.

-!- CAPALYTICATION OF THE VISUAL. SIGNAL.

-!- CAPALYTICATION OF THE VISUAL. SIGNAL.

-!- CAPALYTICATION OF THE VISUAL.

-!- SUBUNIT: OLIGOMER COMPOSED OF TWO CATALYTIC CHAINS (ALPHA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pittler S.J., Baehr W., Dryja T.P., Wasmuth J.J., McConnell D.G., Champagne M.S., Grondin V., Vantuinen P., Ledbetter D., Davis R.L.; "Molecular characterization of human and bovine rod photoreceptor cGMP phosphodiesterase alpha-subunit and chromosomal localization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BETA), AN INHIBITORY CHAIN (GAMMA) AND THE DELTA CHAIN.
DISEASE: DEFECTS IN PDE6A ARE A CAUSE OF AUTOSOMAL DOMINANT
RETINITIS PIGMENTOSA (ADRP) OR AUTOSOMAL RECESSIVE RP (ARRP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-400-1990 (Rel. 15, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Rod cGMP-specific 3, 5'-cyclic phosphodiesterase alpha-subunit (EC 3.1.4.17) (GMP-PDE alpha) (PDE V-B1)
                                                                                                                                                                                                                                                                                                                                                                                                                                   IFDRNRKDELPRLQLEWIDSICMPLYQALVKVNVKLKPMLDSVATNRSKWE
                                                                                                                                                                                                                                                                                         QSEGHNIFANLSSKEYSDLMQLLKQSILATDLTLYFERRTEFFELVSKGE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96083603; PubMed=7493036;
Huang S.H., Pittler S.J., Huang X., Oliveira L., Berson E.L.,
Dryja T.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pittler S.J., Baehr W., Wasmuth J.J., McConnell D.G.,
Champagne M.S., Vantuinen P., Ledbetter D., Davis R.L.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               859 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE-90169986; PubMed-2155175;
                                                                     339 KAEVD---KFK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Senomics 6:272-283(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REVISION TO 845-848.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDE6A OR PDEA.
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ME_Pplase_HDc.
PDEase.
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InterPro; IPR003018; GAF.
InterPro; IPR003607; ME_P!
InterPro; IPR002073; PDEa
                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                            Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from a cDNA clone.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9913;
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P16586;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                215 NFANLIMKWYHLSYLHNCETRRGQILLMSGSKVFEELTDIERQFHKALYTVRAFLNCDRY 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        390 VNKKEEIVGVATFYNRKDGKPFDEMDETLMESLTQFLGWSVLNPDTYESMNKLENRKDIF 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----KESME 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          268 WNSNHQIIGVAQVLNRLDGKPFDDADQRLFEAFVIFCGLGINNTIMYDQVKKSWAKQSVA 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----FKAANIPLVSELAIDDIHFDD 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 FSLDVDAMITAALRMFMELGMVQKFKIDYETLCRWLLIVRKNYRMVLYHNWRHAFNVCQL 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              426 MFAMLTTAGFQDILTEVEILAVIVGCLCHDLDHRGTNNAFQAKSGSALAQLYGTSATLEH 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                330 VIPNPPPDHWALVSGLPAYVAQNGLICNIMNAPAEDFFAFQKEPLDESGWMIKNVLSMPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---KSSYSDWLINNSIAELVASTGLPVNISDAYQDPRFDAEADQI--SGFHIRSVLCVPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87; Gaps
                                  VISION AS WELL. SIMILARITY: BELONGS TO THE CYCLIC NUCLECTIDE PHOSPHODIESTERASE
                        LOOSE THEIR FAR PERIPHERAL VISUAL FIELD AND EVENTUALLY CENTRAL
                                                                                                 WWW-"http://www.retina-international.com/sci-news/pdemut.htm".
PATIENTS TYPICALLY HAVE NIGHT VISION BLINDNESS AND LOSS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 29.8%; Score 1047.5; DB 1; Length Best Local Similarity 32.9%; Pred. No. 2.5e-62; Matches 232; Conservative 136; Mismatches 251; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVLLLEDIESPVVKFTKSFEL - - - - - - - - MSPKCSADAENSF - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                              S -> R (IN ARRP).
/FTId=VAR_006049.
983C361334D58414 CRC64;
                                                                      DATABASE: NAME-Mutations of the PDE6A/B/G genes; NOTE-Retina International's Scientific Newsletter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FARNESYL (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00126; PDEASE_I; 1.
Hydrolase; CGMP; Vision; Prenylation; Lipoprotein;
Retinitis pigmentosa; Disease mutation.
NIT_MET 0 0
            FIELD; AS THEIR
                                                                                                                                                                                                                                                                MIW; 180071; ...
InterPro: IPR003019; GAF.
InterPro: IPR003010; ME_Pplase_HDC.
InterPro: IPR002073; PDEASe.
InterPro: IPR001230; Prenyl_site.
Pfam; PF00233; PDEASe; 1.
Pfam; PF01590; GAF; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          328 LDVLSYHATCSKAEVDK-----
                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00387; PDIESTERASE1.
SMART; SM00065; GAF; 2.
SMART; SM00471; HDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99503 MW;
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                                                                                                                                                                                                                                                  Genew; HGNC:8785; PDE6A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 856
343
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--KGEYDWN-----IKNHRDIFRSMLMTACDLGAVTKPWEISRQVAELVTSEFFEQGDRE 595
                                                                                                                                                                                                                                                                                                                                                             TYESEQEWTQYMMLEQTRKEIVMAMMMTACDLSAITKPWEVQSQVALLVAAEFWEQGDLE 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                 RLELKLTPSAIFDRNRKDELPRLQLEWIDSICMPLYQALVKVNVKLKPMLDSVATNRSKW 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HHFNHAVMILQSEGHNIFANLSSKEYSDLMQLLKQSILATDLTLYFERRTEFFELVS---
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Li T., Volpp K., Applebury M.L.;
"Bovine cone photoreceptor cGMP phosphodiesterase structure deduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [2]
SEQUENCE OF 308-502 FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-90115859; PubMed-2153290;
Charbonneau H., Pursti K.K., Letrong H., Sonnenburg W.K.,
Mullaney P.J., Walsh K., Beavo J.A.;
"Identification of a noncatalytic cGMP-binding domain conserved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 87:288-292(1990).
-!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)0 = guanosine 5'-phosphate.
-!- SUBUNIT: COMPOSED OF TWO ALPHA' SUBUNITS THAT ARE ASSOCIATED WITH 3 SWALLER PROTEINS OF 11, 13, AND 15 kDa.
-!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Cone CGMP·specific 3', cyclic phosphodiesterase alpha'-subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           both the cGMP-stimulated and photoreceptor cyclic nucleotide phosphodiesterases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --EELHQKRLLASTASSS-----SPASVMVAK 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KALADEYDAKMKVQEEKKQKQQSAKSAAAGNQPGGNPSPGGATTSK
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NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                        QIIGVAQVLNRLDGKPFDDADQRLFEAFVIFCGLGINNTIMYDQVKKSWAKQSVALDVLS 332
                                                                                                                                                                                                                                                                                                                                                                                                                      LTTAGFQDILTEVEILAVIVGCLCHDLDHRGTNNAFQAKSGSALAQLYGTSATLEHHHFN 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | ::| :|||||| || || EEEAIKYVTIDPTKKEIIMAMMMTACDLSAITKPWEVQSQVALLVANEFWEQGDLERTVL 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         600 KLTPSAIFDRNRKDELPRLQLEWIDSICMPLYQALVKVNVKLKPMLDSVATNRSKWEEL 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    632 YSKTLLQDESLNIFONLNKRQYETVIHLFEVAIIATDLALYFKKRTMFQKIVDACEKMET
                                                                                                                                                    213 SFVSIILKLHHTNYLYNIESRRSQILMWSANKVFEELTDVERQFHKALYTVRTYLNCERY
                                                                                                                                                                                                                     SVLLL-----EDIESPVVKFTKSFELMSPKCSADAENSF------KESME---KS
                                                                                                                                                                                                                                    SYSDWLINNSIAELVASTGLPVNISDAYQDPRFDAEADQI -- SGFHIRSVLCVPIWNSNH
                                                                                                                                                                                                                                                                                                                                                                                                                                 54 KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYL
                                                                                                                                                                                                                                                                                                                                         333 YHATCSKAEVD---KFK-AANIPLVSELA-------IDDIHFDDFSLD
                                                                                                                                                                                                                                                                                                                                                             NHTKATPDEIKSILKFKEKLNIDVIEDCEEKQLVTILKEDLPDPRTADLYEFRFRHLPIT
                                                                                                                                                                                                                                                                                                                                                                                370 VDAMITAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLYHNWRHAFNVCQLMFAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAVMILQSEGHNIFANLSSKEYSDLMQLLKQSILATDLTLYFERRTEFFELVSKGE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----YDWNIKNHRDIFRSMLMTACDLGAVTKPWEISRQVAELVTSEFFEQGDRERLEL
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                      57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1989 (Rel. 12, Created)
01-NGC-1990 (Rel. 15, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Rod cGMP-specific 3,5'-cyclic phosphodiesterase alpha-subunit
(EC 3.1.4.17) (GMP-PDE alpha) (PDE V-B1).
                                                                                                   Length 855;
                                                                     GERANYL-GERANYL (BY SIMILARITY)
1FCFFFD045686D65 CRC64;
                                                                                                                     234; Conservative 119; Mismatches 249; Indels
                           SMART; SM00065; GAF; 2.
SMART; SM00471; HDc; 1.
PROSITE; PS00126; PDEASE_I; 1.
Hydrolase; cGMP; Vision; Prenylation; Lipoprotein;
                                                                                                29.6%; Score 1039.5; DB 1; 35.5%; Pred. No. 8.5e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             858 AA
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Pfam; PF00233; PDEase; 1.
Pfam; PF01590; GAF; 2.
PRINTS; PR00387; PDIESTERASE1.
                                                                              855 AA; 98797 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovidae: Bovinae: Bos
                                                                                                             Local Similarity
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                                                                               SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence of the alpha-subunit and nucleotide sequence of corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ovchinnikov Y.A., Gubanov V.V., Khramtsov N.V., Ischenko K.A., Zagranichny V.E., Muradov K.G., Shuvaeva T.M., Lipkin V.M.; "Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence of the alpha-subunit and nucleotide sequence of the corresponding
                                                   Pittler S.J., Baehr W., Massmuth J.J., McConnell D.G., Champagne M.S. Vantuinen P., Ledbetter D., Davis R.L.; Molecular characterization of human and bovine rod photoreceptor cGMP phosphodiesterase alpha-subunit and chromosomal localization of the human gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- FUNCTION: THIS PROTEIN PARTICIPATES IN PROCESSES OF TRANSMISSTON AND AMPLIFICATION OF THE VISUAL SIGNAL.
-i- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)0 = guanosine 5'-phosphate.
-i- SUBGNIT: OLIGOMER COMPOSED OF TWO CATALYTIC CHAINS (ALPHA AND BETA), AN INHIBITORY CHAIN (GAMMA) AND THE DELTA CHAIN.
-i- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                 Yu A., Ovchinnikov A., Gubanov V.V., Khramtsov N.V.,
Akhmedov N.B., Ishchenko K.A., Zagranichnyi V.E.,
Vasilevskaya I.A., Fakitina T.V., Atabekova N.V., Barinov A.A.,
Muradov K.G., Shuvaeva T.M., Bystrov N.S., Severtsova I.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDEASE_1; 1. Vision; Lipoprotein; Acetylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACETYLATION.
FARNESYL (BY SIMILARITY).
M -> V.
V -> A (IN REF. 2 AND 3).
T -> A (IN REF. 2 AND 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cyclic GMP phosphodiesterase from the bovine retina.
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-> A (IN REF. 2 AND
-> A (IN REF. 2 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dokl. Akad. Nauk SSSR 296:487-491(1987).
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Interpro; IPR002073; PDEase.
Interpro; IPR001230; Prenyl_site.
SEQUENCE FROM N.A.
MEDLINE=90169986; Pubmed=2155175;
                                                                                                                                                                                                                                                                                                                                TISSUE-Retina;
MEDLINE-88082056; PubMed-2826095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-88030033; PubMed-2822478;
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SMART: SM00065; GAF: 2.
SMART: SM00471; HDC; 1.
PROSITE; PS00126; PDEASE_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEBS Lett. 223:169-173(1987).
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EMBL, MA7541, AAA30441.1; --
EMBL, M36683; AAA30442.1; --
EMBL, M26043; AAA30443.1; --
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Pfam; PF01590; GAF; 2.
                                                                                                                                                                                                                                   Genomics 6:272-283(1990).
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PIR; A34611; A34611.
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MEDLINE-91130581; PubMed-1847109;
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Matches 22
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RRYAYAYA
BRAKKHAHA
BODBA BODB
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                                                                                                                                           54 KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYL 113
                                                                                                                                                                                                                             PFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC 173
                                                                                                                                                                   WNSNHQIIGVAQVLNRLDGKPFDDADQRLFEAFVIFCGLGINNTIMYDQVKKSWAKQSVA
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                                                                                                                                                                                                                                                                                                                                                                                                                      390 VNKKEEIVGVATFYNRKDGKPFDEMDETLMESLTQFLGWSVLNPDTYELMNKLENRKDIF
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-GCT-2001 (Rel. 40, Last annotation update)
Rod cGMP-specific 3',5'-cyclic phosphodiesterase alpha-subunit (EC 3.1.4.17) (GMP-PDE alpha).
                                                                                                     80;
                                                                                                                                                                                                                                                                                                             SVLLLEDIESPVVKFTKSFEL------MSPKCSADAENSF-----
                                                                                                     Conservative 138; Mismatches 248; Indels
                                                              Length
F -> C (IN REF. 2 AND 3).
86624E43662A95CC CRC64;
                                                            Score 1030; DB 1;
Pred. No. 3.7e-61;
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                   99209 MW;
                                                            29.3%;
                                                                                 32.68;
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                 858 AA;
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                 SEQUENCE
                                                            Query Match
                                                                                 Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----KESME 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---KSSYSDWLINNSIAELVASTGLPVNISDAYQDPRFDAEADQI--SGFHIRSVLCVPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 NFVNLIMKVFHLSYLHNCETRRGQILLWSGSKVFEELTDIERQFHKALYTVRAFLNCDRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QDIVKYHVKCDNEEIQKILKTREVYGKEPWECEEEELAEILQRELPDAESYEINKFHFSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                -!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)0 = guanosine 5'-phosphate.
-!- SUBUNIT: OLIGOMER COMPOSED OF TWO CATALYTIC CHAINS (ALPHA AND BETA), AN INHIBITORY CHAIN (GAMMA) AND THE DELTA CHAIN.
-!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE FAMILY.
                                                                                            -, a putative beta-subunit isozyme produced by alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80;
Baehr W., Champagne M.S., Lee A.K., Pittler S.J.; "Complete cDNA sequences of mouse rod photoreceptor cGMP phosphodiesterase alpha- and beta-subunits, and identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVLLLEDIESPVVKFTKSFEL - - - - - - MSPKCSADAENSF - - -
                                                                                                                             splicing of the beta-subunit gene.";
FEBS Lett. 278:107-114(1991).
-!- FUNCTION: THIS PROTEIN PARTICIPATES IN PROCESSES OF
- TRANSMISSION AND AMPLIFICATION OF THE VISUAL SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FARNESYL (BY SIMILARITY).
E29A626B23F7DDA0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase; cGMP; Vision; Prenylation; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.7e-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.3%; Score 1030; DF 32.9%; Pred. No. 3.7e-iive 133; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDVLSYHATCSKAEVDKFKAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:97524; Pde6a.
InterPro; IPR003018; GAF.
InterPro; IPR003007; ME_Pplase_HDC.
InterPro; IPR0030073; PDEase.
InterPro; IPR001230; Prenyl_site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS, PR00387; PDIESTERASE1.
SMART; SM00065; GAF; 2.
SMART; SM00471; HDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00126; PDEASE_I; 1.
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EMBL;
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                  MFAMLTTAGFQDILTEVEILAVIVGCLCHDLDHRGTNNAFQAKSGSALAQLYGTSATLEH 485
                                                                                                                                                                                           ----YDWN-----IKNHRDIFRSMLMTACDLGAVTKPWEISRQVAELVTSEFFEQGDRE 595
                                           HHFNHAVMILQSEGHNIFANLSSKEYSDLMQLLKQSILATDLTLYFERRTEFFELVSKGE
                                                                                                                                                                                                                                                                                RLELKLTPSAIFDRNRKDELPRLQLEWIDSICMPLYQALVKVNVKLKPMLDSVATNRSKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Gene structure and amino acid sequence of the human cone photocraceptor cGMP-phosphodiesterase alpha' subunit (PDEA2) and its chromosomal localization to 10q24."; Genomics 28:429-435(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feshchenko E.A.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
-!-CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)O = quanosine 5'-phosphate.
-!- SUBUNIT: COMPOSED OF TWO ALPHA' SUBUNITS THAT ARE ASSOCIATED WITH 3 SMALLER PROTEINS OF 11, 13, AND 15 kDa.
-!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cone cGMP-specific 3',5'-cyclic phosphodiesterase alpha'-subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Piriev N.I., Viczian A.S., Ye J., Kerner B., Korenberg J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A., Ye J., Farber D.;
to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                          -- EELHQKRLLASTASSSS 672
                                                                                                                                                                                                                                                                                                                                                                                                                 KALADEYEAKMKALEEEKQKQQAAKQAASGN 839
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EMBL; U20196; AAA92886.1; JOINED.
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Piriev N.I., Viczian
Submitted (MAY-1995)
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PDE6C OR PDEA2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYL
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V -> D (IN REF. 3).
Q -> P (IN REF. 3).
Q -> P (IN REF. 1).
P -> L (IN REF. 1).
P -> L (IN REF. 1).
W, 3D1535C21780A56E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 858;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29.3%; Score 1029.5;
34.7%; Pred. No. 4e-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; cGMP; Vision; Prenylation;
                                                                                                                                                                                                                                                                                                              InterPro; IPR003607; ME_Pplase_HDc.
InterPro; IPR002073; PDEase.
InterPro; IPR001230; Prenyl_site.
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SMART; SM00065; GAF; 2.
SMART; SM00471; HDC; 1.
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                                                                                                                                                                                          Li, U20210; AAA92886.1; JT
Li, U20211; AAA92886.1; JT
Li, X94354; CAA64079.1;
ew; HGNC; PDE6C.
  AAA92886.1;
                                                            AAA92886.1;
                      AAA92886.1;
                                         AAA92886.1;
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AAA92886.1;
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858 P
                                       U20202;
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Best Local Simi
Matches 229;
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                                                                                                        KLTPSAIFDRNRKDELPRLQLEWIDSICMPLYQALVKVNVKLKPMLDSVATNRSKWEEL 658
                                                                                                                                         815
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93248211; PubMed=8387203; Suber M.L., Pittler S.J., Qin N., Wright G.C., Holcombe V., Lolee R.L., Craft C.M., Lolley R.N., Baehr W.B., Hurwitz R.L., millsh setter dogs affected with rod/cone dysplasia contain a nonsense mutation in the rod cGMP phosphodiesterase beta subunit gene."; Proc. Natl. Acad. Sci. U.S.A. 90:3968-3972(1993).
| ::| :||:||||| | EEBAIKYVTVDPTKKEIIMAMMMTACDLSAITKPWEVQSQVALMVANEFWEQGDLERTVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (RCD1)
                                             ----YDWNIKNHRDIFRSMLMTACDLGAVTKPWEISRQVAELVTSEFFEQGDRERLEL
                                                                                                                       FUNCTION: THIS PROTEIN PARTICIPATES IN PROCESSES OF TRANSMISSION AND AMPLIFICATION OF THE VISUAL SIGNAL. NECESSARY FOR THE FORMATION OF A FUNCTIONAL PHOSPHODIESTERASE HOLOENZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate +H(2)0 = quanosine 5'-phosphate +H(2)0 = quanosine 5'-phosphate +H(2)0 = guanosine 5'-phosphate +H(2)0 = guanosine 5'-phosphate +H(2)0 = guanosine 5'-phosphate ComPose OF TWO CATALYTIC CHAINS (ALPHA AND BETA), AN INHIBITORY CHAIN (GAMMA) AND THE DELTA CHAIN.
-!- SUBCELLUAR LOCATION: Membrane-associated
-!- DISEASE: IRISH SETTER DOGS AFFECTED WITH ROD/CONE DYSPLASIA (RC CONTAIN A NONSENSE MUTATION IN THE GENE THAT GIVES RISE TO A PROTEIN OF 807 AA LACKING 49 AA IN THE C-TERMINAL.
-!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                              01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
115-UTL-1998 (Rel. 36, Last annotation update)
Rod cGMP-specific 3',5'-cyclic phosphodiesterase beta-subunit
EC 3.1.4.17) (GMP-PDE beta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRALPBOXER X Doberman; TISSUE-Retina;
Clements P.J.;
Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                     856 AA
                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; 334230; 334230.
InterPro: IPR003018; GAF.
InterPro: IPR003607; WE.Pplase_HDc.
InterPro: IPR002073; PDEase.
InterPro: IPR001230; Prenyl_site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L13262; AAA30882.1; ALT_SEQ
PIR; S34290; S34290.
                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Red setter; TISSUE-Retina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00233; PDESSE; 1.7-Pfam; PF01590; GAF; 2. PRINITS; PR01890; GAF; 2. SMART; SM00065; GAF; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z23014; CAA80557.1; -.
                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                              familiaris (Dog)
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9615;
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                                                                                                                                                                                                                                                                                                                                        EKVMQMYLPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQ 165
                                                                                                                                                                                                                                                                                                                                                                                                                207
                                                                                                                                                                                                                                                                                                                                                                                                                                        321 LHGKEDIKVIPSPPADHWALASGLPTYVAESGFICNIMNTAADEMFTFQEGPLDDSGWVI 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSVLCVPIWNSNHQIIGVAQVLNRLDGKPFDDADQRLFEAFVIFCGLGINNTIMYDQVKK 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWAKQSVALDVLSYHATCSKAEVDKFKAAN-------IPLVSELA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    441 LENRKDIAQDMVLYHVRCDKDEIQLILPTRERLGKEPADCEEDELGILLKEVLPGPSKFD 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---KESME--KSSYSD-WLINNSIAELVASTGLPVNISDAYQDPRFDAEADQI--SGFHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELVTSEFFEQGDRERLELKLTPSAIFDRNRKDELPRLQLEWIDSICMPLYQALVKVNVKL
                                                                                                                                                                                                                                                                                                                                                                                                                  TLLKCERCSVLLLEDIESPVVKFTKSFEL------MSPKCSADAENSF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDDIHFDDFSLDVDAMITAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLYHNWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTSATLEHHHFNHAVMILQSEGHNIFANLSSKEYSDLMQLLKQSILATDLTLYFERRTEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     538 FELVSKGEYDWNIKNHRD------IFRSMLMTACDLGAVTKPWEISRQVA
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                                                                                                          SIMILARITY).
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P35913; Q9BWH5;
01-JUN-1994 (Rel. 29, Created)
01-JUN-2002 (Rel. 29, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Rod coMP-specific 3',5'-cyclic phosphodiesterase beta-subunit (EC 3.1.4.17) (GMP-PDE beta).
PDEGB OR PDEB.
                                                                                                                             GERANYL-GERANYL (BY SIMILARITY)
AC9D03F64D1BA132 CRC64;
                                     Membrane;
                                                                      ROD CGMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE BETA-SUBUNIT. REMOVED IN MATURE FORM (BY SIMI
                                                                                                                                                                                                                          Matches 231; Conservative 125; Mismatches 243; Indels
                                                                                                                                                                                    Length
             PROSITE; PS00126; PDEASE_I; 1.
Hydrolase; cGMP; Vision; Prenylation; Lipoprotein;
                                                                                                                                                                                    DB 1;
                                                                                                                                                                         Score 1024; DB 1,
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                                                                                                                                               98461 MW;
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                                                                                                                                                                                    29.1%;
34.1%;
SMART; SM00471; HDC; 1.
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                                                                                                                                               856 AA;
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                                                       Disease mutation
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853
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                                                                        CHAIN
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"The human beta subunit of rod photoreceptor GGMP phosphodiesterase: complete retinal cDNA sequence and evidence for expression in brain."; Genomics 13:698-704(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      its localisation to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gal A., Orth U., Bachr W., Schwinger E., Rosenberg T., "Heterozygous missense mutation in the rod cGMP phosphodiesterase beta-subunit gene in autosomal dominant stationary night blindness."; Nat. Genet. 7:64-68(1994).
                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                               Khramtsov N.V., Feshchenko E.A., Suslova V.A., Terpugov B.E., Rakitina T.V., Atabekova N.V., Shmukler B.E., Lipkin V.M.; "Structural studies of cDNA and the gene for the beta-subunit of phosphodiesterase from human relina."; Bioorg. Khim. 18:1551-1554(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B., Kowbel D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human gene
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MEDLINE=93350628; PubMed=8394174;

McLaughlin M.E., Sandberg M.A., Berson E.L., Dryja T.P.;

"Recessive mutations in the gene encoding the beta-subunit phosphodisesterase in patients with retinitis pigmentosa.";

Nat. Genet. 4:130-134(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Collins C., Lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genomic organization and complete sequence of the the beta-subunit of the cGMP phosphodiesterase and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95038845; Pubmed=7951329;
Gal A., Orth U., Baehr W., Schwinger E., Rosenberg
Nat. Genet. 7:551-551(1994).
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Andrew S., Schappert K., Hayden M.R.;
                                                                                                                                                                                                                                                TISSUE=Retina;
MEDLINE=93244036; PubMed=1338685;
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                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Retina;
MEDLINE=92347868; PubMed=1322354;
                                                                                                                MEDLINE=93351644; PubMed=8394243;
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MEDLINE=96330350; PubMed=8768262;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cyclic GMP phosphodiesterase.";
Bioorg. Khim. 22:256-263(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 238-854 FROM N.A.
                                                                                                                                                                                                 FEBS Lett. 327:275-278(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT CSNB3 ASN-258.
sapiens (Human)
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                               FROM N.A.
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                                                NCBI_TaxID=9606;
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VARIANT ARRP ASP-576.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Valverde D., Baiget M., Seminago R., del Rio E., Garcia-Sandoval B., del Rio T., Bayes M., Balcells S., Martinez A., Grinberg D., Ayuso C.; "Identification of a novel R5520 mutation in exon 13 of the beta-subunit of rod phosphodiesterase gene in a Spanish family with autosomal recessive retinitis pigmentosa."; Hum. Mutat. 8:393-394(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDITINE—98205225; Pubmed=9543643;
Saga M., Mashima Y., Akeo K., Kudoh J., Oguchi Y., Shimizu N.;
Saga M., Mashima Y., Akeo K., Kudoh J., Oguchi Y., Shimizu N.;
"A novel homozygous Ile535Asn mutation in the rod cGMP
phosphodiesterase beta-subunit gene in two brothers of a Japanese
family with autosomal recessive retinitis pigmentosa.";
Curr. Eye Res. 17:332-335(1998).
-!- FUNCTION: THIS PROTEIN PARTICIPATES IN PROCESSES OF
TRANSMISSION AND AMPLIFICATION OF THE VISIAL SIGNAL. NECESSARY
FOR THE FORMATION OF A FUNCTIONAL PHOSPHODIESTERASE HOLOENZYME.
                                                                                                                                                                                                                                                                                                                         Α,
                                                                                                                                                         Gao Y.Q., Danciger M., Zhao D.Y., Blaney J., Piriev N.I., Shih J., Jacobson S.G., Heckenlively J.H., Farber D.B.; "Screening of the PDESB gene in patients with autosomal dominant retinitis pigmentosa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                       "A novel mutation in exon 17 of the beta-subunit of rod phosphodiesterase in two RP sisters of a consanguineous family."; Hum. Genet. 97:35-38(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WWW="http://www.retina-international.com/sci-news/pdemut.htm"
                                                                                                                                                                                                                                                                                                     Valverde D., Solans T., Grinberg D., Balcells S., Vilageliu L., Bayes M., Chivelet P., Besmond C., Goossens M., Gonzalez-Duarte
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MEDLINE=96129294; PubMed=8595886; Danciger M., Blaney J., Gao Y.Q., Zhao D.Y., Heckenlively J.R Jacobson S.G., Farber D.B.; "Mutations in the PDE6B gene in autosomal recessive retinitis pigmentoes ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DATABASE: NAME-Mutations of the PDE6A/B/G genes; NOTE-Retina International's Scientific Newsletter;
                                                                                                                         VARIANTS ADRP LYS-166; HIS-212 AND HIS-228
                                                                                                                                            MEDLINE=96273603; PubMed=8698075;
                                                                                                                                                                                                                                                                                      MEDLINE=96140746; PubMed=8557257;
                                                                                                                                                                                                                                                                                                                                                                                                                                VARÍANT ARRP GLN-552.
MEDLINE=97114306; PubMed=8956055;
                                                                                                                                                                                                                                  Eye Res. 62:149-154(1996).
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                                                                                       Genomics 30:1-7(1995).
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                                                                                                                                                                                                                                                                     VARIANT ARRP ARG-699
                                                                       pigmentosa.
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513 ELDLVKCGIOMYYELGVVRKFQIPOEVLVRFLFSISKGYRRITYHNWRHGFNVAOTMFTL 572
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453 LYHVKCDRDEIQLILPTRARLGKEPADCDEDELGEILKEELPGPTTFDIYEFHFSDLECT 512
                                                             370 VDAMITAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLYHNWRHAFNVCQLMFAM 429
                                                                                                                                                                                      LTTAGFQDILTEVEILAVIVGCLCHDLDHRGTNNAFQAKSGSALAQLYGTSATLEHHHFN 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   490 HAVMILQSEGHNIFANLSSKEYSDLMQLLKQSILATDLTLYFERRTEFFELVSKGEYDWN
                                                                                                                                                                                                                                                                                                                                                  ----IFRSMLMTACDLGAVTKPWEISRQVAELVTSEFFEQGD
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DISEASE: DEFECTS IN PDE6B ARE THE CAUSE OF RETINAL DEGENERATION. SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE FAMILY.
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"Complete cDNA sequences of mouse rod photoreceptor CGMP
phosphodiesterase alpha- and beta-subunits, and identification of
beta'., a putative beta-subunit isozyme produced by alternative
splicing of the beta-subunit gene.";
FEBS Lett. 278:107-114(1991).
TRANSMISSION AND AMPLIFICATION OF THE VISUAL SIGNAL. NECESSARY
FRANSMISSION AND AMPLIFICATION OF THE VISUAL SIGNAL. NECESSARY
FOR THE FORMATION OF A FUNCTIONAL PHOSPHODIESTERASE HOLOENZYME.
-:- CATALVITC ACTIVITY: Gamoosine 3',5'-cyclic phosphate + H(2)O =
guanosine 5'-phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the rd mouse is caused by a defect in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: OLIGOMER COMPOSED OF TWO CATALYTIC CHAINS (ALPHA AND BETA), AN INHIBITORY CHAIN (GAMMA) AND THE DELTA CHAIN. SUBCELLULAR LOCATION: Membrane-associated.
ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2/Beta';
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-2002 (Rel. 41, Last annotation update)
Rod cGMP-specific 3',5'-cyclic phosphodiesterase beta-subunit (EC 3.1.4.17) (GMP-PDE beta)
PDE6B OR PDE8 OR PDE 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6; TISSUE=Retina;
MEDLINE=91015387; PubMed=1977087;
Bowes C., Li T., Danciger M., Baxter L.C., Applebury M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 beta subunit of rod cGMP-phosphodiesterase.";
Nature 347:677-680(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 856 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91130581; PubMed=1847109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Retinal degeneration in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                      550 IKNHRD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KWEEL 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1991 (Rel.
01-NOV-1991 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Retina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Farber D.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CNRB_MOUSE
                                                                                                                                                                                      430
                                                                                                                                                                                                                                                                                                                                                                         632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEDIESPVVKFTKSFELMS------PKCSADAENSF------KESME---K 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LD-----MTKEKEFFDVWSVLMGESQPYSGPRTPDGREIVFYKVIDYILHGKEEIKVIPT 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 FNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYLPFCG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSYSDWLINNSIAELVASTGLPVNISDAYQDPRFDAEADQI--SGFHIRSVLCVPIWNSN 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HQIIGVAQVLNRLDGKPFDDADQRLFEAFVIFCGLGINNTIMYDQVKKSWAKQSVALDVL 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMART: SMO065; c...
SMART: SM00471; HDc; 1.
PROSITE; PS00126; PDEASE_I; 1.
PROSITE; PS00126; PDEASE_I: 1.
Hydrolase; cGMP; Vision; Prenylation; Lipoproce....
Rydrolase; cGMP; Vision; Prenylation.
Retinitis pigmentosa; Disease mutation.
Retinitis pigmentosa; Disease mutation.
PHOSPHODIESTERASE BETA-SUBUNIT.
PHOSPHODIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 854;
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/FTId=VAR_009286.
L -> H (IN ADRP AND ARRP).
/FTId=VAR_009287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ed. No. 1.7e-60;
Mismatches 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1020; DB 1;
Pred. No. 1.7e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R -> C (IN ARRP).
/FTId=VAR_009283.
E -> K (IN ADRP).
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Y -> H (IN ADRP).
/FTId=VAR_009285.
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H -> N (IN CSNB3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro: IPR003018; GAF.
InterPro: IPR003057; ME_Pplase_HDc.
InterPro: IPR002073; PDEase.
InterPro: IPR001230; Prenyl_site.
Pfam; PF00233; PDEase; 1.
Pfam; PF00237; PDESTERASE1.
SMART; SW00065; GAF; 2.
SMART; SW00065; GAF; 2.
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                   CAA44569.1)
CAA44569.1)
CAA44569.1,
CAA44569.1,
CAA62215.1,
CAA622
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29.0%; Soc
Best Local Similarity 34.4%; Pro
Matches 229; Conservative 118;
                                                                                                                                                                                                                                                                    ; BC000249; AAH00249;1;
A42828; A42828.
S34590; S34590.
                                                                                                                                                                                                                                                                                                                                     14590; S34590.
HGNC:8786; PDE6B.
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                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 268000; 7.
MIM; 163500; 7.
                                                                                                                                               X90587;
X90588;
X90589;
                                                                                       X62694;
X62695;
                                                          X62693;
                                                                                                                                                                                                                                             x90590;
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EMBL; Z68340; CAA92763.1; -. EMBL; U52868; AAB70037.1; -.
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                                                                                                                                                                                                                                                                                                                                    Canis familiaris (Dog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Retina;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Hurwitz R.L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266 AYLNCERYSVGLLD-----MTKEKEFFDVWPVLMGEAQPYSGPRTPDGREIVFYKVIDYI 320
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                                                                                                                                                                                                                                                                                  ROD CGMP-SPECIFIC 3',5'-CYCLIC
PHOSPHODIESTERASE BETA-SUBUNIT.
REMOYED IN MATURE FORM (BY SIMILARITY).
MISSING (IN ISOFORM 2).
G -> E (IN REF. 2).
S -> A (IN REF. 2).
DV -> EL (IN REF. 2).
T -> P (IN REF. 2).
T -> P (IN REF. 2).
C -> L (IN REF. 2).
C -> E (IN REF. 2).
S -> G (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206 EDVFTKYLNFATLNLKIYHLSYLHNCRTRRSQVLLWSANKVFEELTDIERQFHKAFYTVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----KFKAANIPLVSELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---KESME---KSSYSDWLINNSIAELVASTGLPVNISDAYQDPRFDAEADQI--SGFHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RSVLCVPIWNSNHQIIGVAQVLNRLDGKPFDDADQRLFEAFVIFCGLGINNTIMYDQVKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        358 IDDIHFDDFSLDVDAMITAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLYHNWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      166 TLLKCERCSVLLLEDIESPVVKFTKSFEL------MSPKCSADAENSF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78;
                                                                                                                                                                                                                                                    PROSITE; PSO0126; PDEASE_1; 1.
Hydrolase; cGMP; Vision; Prenylation; Lipoprotein; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                29.0%; Score 1020; DB 1; Length 856; 34.0%; Pred. No. 1.7e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           3677704D0C7496D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative 121; Mismatches 248;
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                                                                                                                                  MGD; MGI:9725; Pde6b.
InterPro; IPR003018; GAF.
InterPro; IPR003607; ME_Pplase_HDC.
InterPro; IPR002073; PDEase.
InterPro; IPR001230; Prenyl_site.
Pfam; PF00233; PDEase; 1.
Pfam; PF01590; GAF; 2.
                                                                                                 EMBL; X55968; CAA39439.1; ALT_SEQ.
EMBL; X60133; CAA42719.1; -.
PIR; S13121; S13121.
                                                                                                                                                                                                              PRIMI, F. PRO0387; PDIESTERASE1.
SMART; SM00065; GAF; 2.
SMART; SM00471; HDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                           98501 MW;
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                                                                                                                                                                                                                                                                                                                                                                   50
158
176
232
236
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232
236
856 AA;
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Best Local Similarity
Matches 230; Conserv
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853
801
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49
158
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CONFLICT
CONFLICT
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561 HGFNVAQTMFTLLMTGKLKSYYTDLEAFAMVTAGLCHDIDHRGTNNLYQMKSQNPLAKLH 620
                                                                                                                                                                                                                                                                                                                                                                680 QKIVDES-----KNYEDKKSWVEYLSLETTRKEIVMAMMTACDLSAITKPWEVQSKVA 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELVTSEFFEQGDRERLELKLTPSAIFDRNRKDELPRLQLEWIDSICMPLYQALVKVNVKL 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDINE-98099662; PubMed-9233984; Wang W., Acland G.M., Aguire G.D., Ray K.; Wang w., Acland G.M., Aguire G.D., Ray K.; "Cloning and characterization of the cDNA encoding the alpha-subunit of CGMP-phosphodiesterase in can
                                                                                                                                                                             G-SSILERHHLEFGKFLLAEESLNIYONLNRRQHEHVIHLMDIAIIATDLALYFKKRTMF
                                                                                                                                                                                                                                                                           ----IFRSMLMTACDLGAVTKPWEISRQVA
                                                                                         GTSATLEHHHFNHAVMILQSEGHNIFANLSSKEYSDLMQLLKQSILATDLTLYFERRTEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-Beagle X Briard; TISSUE-Retina;
Veske A., Nilsson S.E.G., Gal A.;
Veske A., Nilsson S.E.G., Gal A.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN PARTICIPATES IN PROCESSES OF
TRANSMISSION AND AMPLIFICATION OF THE VISUAL SIGNAL.
-!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)O =
-!- SIBUNIT: OLICOMER COMPOSED OF TWO CATALYTIC CHAINS (ALPHA AND
BETA), AN INIBITIONY CHAIN (GAMMA) AND THE DELFA CHAIN.
-!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNRA_CANFA STANDARD; PRT; 860 AA.
028263; 029470;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Rod coMp-specific 3',5'-cyclic phosphodiesterase alpha-subunit (EC 3.1.4.17) (GMP-PDE alpha).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Elevation of cGMP with normal expression and activity of rod cGMP-PDE in photoreceptor degenerate labrador retrievers."; Ophthalmic Res. 28:19-28(1996).
                                                                                                                                                                                                                                                                       FELVSKGEYDWNIKNHRD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96331105; PubMed=8726673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KPMLDSVATNRSKWEEL
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                        "Beta-subunit of bovine rod photoreceptor cGMP phosphodiesterase
                                                                                                                                                                       MEDLINE-90330632; Pubmed-2165490;
Lipkin V. M., Khramtsov N.V., Vasilevskaya I.A., Atabekova N.V.,
Muradov K.G., Gubanov V.V., Li T., Johnston J.P., Volpp K.J.,
Applebury M.L.;
01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Red cGMP-specific 3',5' cyclic phosphodiesterase beta-subunit (EC 3.1.4.17) (GMP-PDE hera)
                                                                                                                                                                                                                                                                                      MEDLINE=90267525; PubMed=2161230;
Lipkin V.M., Gubanov V.V., Khramtsov N.V., Vasilevskaya I.
Atabekova N.V., Muradov K.G., Shuvaeva T.M., Surina E.A.,
                                                                                                                                                                                                                                   Comparison with the phosphodiesterase family.";
J. Biol. Chem. 265:12955-12959(1990).
                                                          (EC 3.1.4.17) (GMP-PDE beta).
PDE6B OR PDEB.
                                                                                    Bos taurus (Bovine).
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                       NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MFAMLTTAGFQDILTEVEILAVIVGCLCHDLDHRGTNNAFQAKSGSALAQLYGTSATLEH 485
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                                                                                                                                                                                                                                                             54 KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYL 113
                                                                                                                                                                                                                                                                                                              114 PFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC 173
                                                                                                                                                                                                                                                                                                                                                                  --KESME 212
                                                                                                                                                                                                                                                                                                                                                                                                               213 ---KSSYSDWLINNSIAELVASTGLPVNISDAYQDPRFDAEADQI--SGFHIRSVLCVPI 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 FSLDVDAMITAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLYHNWRHAFNVCQL 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268 WNSNHQIIGVAQVLNRLDGKPFDDADQRLFEAFVIFCGLGINNTIMYDQVKKSWAKQSVA 327
                                                                                                                                                                                                                                                                            || || : | : | : | : | : | SVGLLD-----MTKQKEFFDVWPVLMGEAPPYSGPRTPDGREINFYKVIDYILHGKEDIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 328 LDVLSYHATCSKAEVDK ------FKAANIPLVSELAIDDIHFDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        450 QDMVKYHVKCDNEEIQKILKTREVYGKEPWECEEEELAEILQGELPDAEKYEINKFHFSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       510 LPLTELELVKCGIQMYYELKVVDKFHIPQEALVRFMYSLSKGYRRITYHNWRHGFNVGQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HHFNHAVMILQSEGHNIFANLSSKEYSDLMQLLKQSILATDLTLYFERRTEFFELVSKG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RLELKLTPSAIFDRNRKDELPRLQLEWIDSICMPLYQALVKVNVKLKPMLDSVATNRSKW
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                      99
                                                                                                                                                                                                               Length 860;
                                                                                                                                                                                                                         al Similarity 33.2%; Pred. No. 2e-60;
220; Conservative 133; Mismatches 244; Indels
                                                                                                  SNART; SM00471; HDC; 1.
PROSITE; PS00126; PDEASE_I; 1.
Hydrolase; CGMP; Vision; Premylation; Lipoprotein.
TWIT MET 0 0 BY SIMILARITY.
FARNESIL (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                SVLLLEDIESPVVKFTKSFEL------MSPKCSADAENSF-
                                                                                                                                                                                   5260B0BC579A25F7 CRC64;
                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                             29.0%; Score 1019; 33.2%; Pred. No. 2e
         InterPro; IPR003018; GAF.
InterPro; IPR003607; ME_Pplase_HDc.
InterPro; IPR002073; PDEase.
InterPro; IPR001230; Prenyl_site.
Pfam; PF00233; PDEase; 1.
Pfam; PF001590; GAF; 2.
PRINTS; PR00387; PDIESTERASE1.
SMART; SM00655; GAF; 2.
SMART; SM006471; HDC; 1.
                                                                                                                                                                                    99557 MW;
EMBL; Y13282; CAA73731.1; -.
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860 AA;
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                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY).
CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)O = quanosine 5'-phosphate  
SUBUNIT: OLIGOMER COMPOSED OF TWO CATALYTIC CHAINS (ALPHA AND BETA), AN INHIBITORY CHAIN (GAMMA) AND THE DELTA CHAIN. SUBCELLULAR LOCATION: Membrane-associated  
SIMILLARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GERANYL-GERANYL (BY SIMILARITY)
DE -> EQ (IN REF. 2).
C4B3F22CFFE7F2FB CRC64;
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Pred. No. 9.2e-60;
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InterPro; IPR003607; ME_Pplase_HDc.
InterPro; IPR002073; PDEase.
InterPro; IPR001230; Prenyl_site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00233; PDEase; 1.
Pfam; PF01590; GAF; 2.
PRINTS; PR00387; PDIESTERASE1.
SMART; SM00055; GAF; 2.
SMART; SM00471; HDc; 1.
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98330
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850
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PIR; S19145; S19145.
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850
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853 AA.

PRT;

STANDARD;

CNRB_BOVIN

q

RESULT 15 CNRB_BOVIN

13;	117	217	177	277	214	332	271	392	331	452	369	512	429	572	489	631	549	989	593	745	653	805		
Gaps	IYLPFCG	YLNFGT	RCSVLL	RYSVGL	KESMEKS	:: I	PIWNSN	II I IPIVNKK	VALDVL	: : IAQDMV	DDFSLD	SDLECT	QLMFAM	OTMFTE	EHHHFN	I II ERHHLE	GEYDWN	S	FFEOGD	FWEOGD	VATNRS	: LQNNRK		
88;	EKVMON	EDVFL	TLLKCE	AYLNCI	KES	LHGKEL	RSVLCV	KNVLS	SWAKQS	:: LENRK	IDDIHE	I : IYEFHF	HAFNVC	HGENVA	GTSATI	G-SSIL	FELVSK	:: : QKIVDE	ELVTSE	: LLVAAE	KPMLDS	II LPMFDR		
Indels	GAPFTEDD	GPCFTSED	KK IMHRAQ	HKAFYTVR		I FYKVIDYI	ISGFHI	LDDSGWIV	IMYDQVKK	DTYDKMNK	KFKAANIPLVSELAIDDIHFDDFSLD	: LPGPAKFD	MVLYHNWR	RITYHNWR	SSALAQLY	: : : ONPLAKLHO	YFERRTEF	:: YFKKRTMF	WEISROVA	II: :II	LVKVNVKL	:::: FSRFHEETI		
244;	INKIPE	VNKL-D	DLEKIV . .	DIERQE	ADAENS	DGREIL	DAEADQ	NFQEGP	LGINNT	SVLNT!	KFKAAN	KILKEV.	VRKNYR	VSKGYR	AFOAKS	LYQMKS	ATDLTL	ATDLAL	SAVTKP	: SAITKP	4PLYQA1	: I : FFVYKEI		•
Mismatches	FNDEIDKLIGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYLPFCG	FSSFADELTDYVTRNILATPIMNGK-DVVAVIMAVNKL-DGPCFTSEDEDVFLKYLNFGT	IAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAQTLLKCERCSVLL	LNIKIYHLSYLHNCETRRGQVLLMSANKVFEELTDIERQFHKAFYTVRAYLNCDRYSVGL	LEDIESPVVKFTKSFELMSPKCSADAENSF		SYSD-WLINNSIAELVASTGLPVNISDAYQDPRFDAEADQISGFHIRSVLCVPIWNSN	PPADHWALASGLFTYVAESGFICNIMNAPADEMFNFQEGFLDDSGWIVKNVLSMPIVNKK	EAFVIFCG	EEIVGVATFYNRKDGKPFDEQDEVLMESLTQFLGWSVLNTDTYDKMNKLENRKDIAQDMV		LYHVRCDREEIQLILPTRERLGKEPADCEEDELGKILKEVLPGPAKFDIYEFHFSDLECT	VDAMITAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLYHNWRHAFNVCQLMFAM	ELELVKCGIQMYYELGVVRKFQIPQEVLVRFLFSVSKGYRRITYHNWRHGFNVAQTMFTL	OLDHRGTNN	LMTGKLKSYYTDLEAFAMVTAGLCHDIDHRGTNNLYQMKSQNFLAKLHG-SSILERHHLE	WILKOSIL.	FGKFLLSEETLNIYQNLNRRQHEHVIHLMDIAIIATDLALYFKKRTMFQKIVDES	SMLMTACDL	-	DEWIDSIC	LERTVLDQQPIPWMDRNKAABLPKLQVGFIDFVCTFVYKEFSRFHEETLPMFDRLQNNRK	AKEDR 683	:11: LEEDQ 825
128; Mis	MPIRSSD(TPIMNGK	SRALLEV	GOVLLWS	1	PVLMGEA(TGLPVNIS	SGFICNIN	DDADQRLE	DEQDEVLA	SYHATCSKAEVD	ERLGKEP?	OKFKIDYE	RKFQIPQE	IVGCLCHI	· VŤAGLCHI	SKEYSDLA	RRQHEHVI	IFRS	IRKEIVM	KDELPRLC	AAELPKLC	KWEELHQKRLLASTASSSPASVMVAKEDR	: : : : :
	KTKSLLC	VTRNILA	SRKEYER	HUCETRR	RSFEL-	: : : KEFFDVW	FAELVAS	PTYVAE	REDGKPF	KDGKPE		LILPTR	MELGMV	YELGVV	SVEILAV	LEAFAM	VIFANLS	NINÖAIN		SYLSLET	AIFDRNE	MMDRNK	STASSS	ADE
Conservative	IDKLTGY	ADELTDY	NAQLFAA:	IXHLSYLI	SPVVKF	MTKE	WLINNS.	WALASGI	SVAQVLNE	SVATFYNE	CSKAEVI	CDREEIC	TAALRME	VKCGIQM	SFQDILT	KLKSYYTI	LLQSEGH	LSEETL	g	I EDRKSWVE	SLKLTPS?	LDQQPIF	HOKRLLA	
			IAIS	LNLK			SYSD	PPAD	HQII	EEIV	SYHA	LYHVI	VDAM	ELEL		LMTG	HAVM	FGKF	IKNHI	- KNY	RERLI	LERT	KWEEI	EWKAL-
230;	58	160	118	218	178	278	215	333	272	393	332	453	370	513	430	573	490	632	550	687	594	746	654	806
Matches																								
	Οy	qq	Qγ	QO	Qy	qa	Ωý	qq	Οy	QQ	Qy	QG	οy	QQ	Οý	qq	ΟŸ	qa	Oy	qq	Qy	QQ	Qy	qa

Search completed: June 13, 2003, 15:47:42 Job time: 17.0228 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

June 13, 2003, 15:49:06 ; Search time 49.0797 Seconds Run on:

(without alignments) 1490.031 Million cell updates/sec

US-09-663-542-1

3516 1 MLKQARRPLFRNVLSATQWK.....ASTASSSSPASVMVAKEDRN 684 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 408643 segs, 106915682 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published_Applications_AA:* Database :

/cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.ppp:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		đ			SUMMAKTES	
Result No.	Score	Query Match	Query Match Length DB	DB	QI .	Description
1	3516	100.0	684	10	US-09-891-216-14	Sequence 14, Appl
7	3250	92.4	934	10	US-09-891-216-12	Sequence 12, Appl
3	3250	92.4	934	10	US-09-891-216-15	Sequence 15, Appl
4	2970	84.5	576	10	US-09-891-216-13	Sequence 13, Appl
'n	2541	72.3	490	σ	US-10-094-168B-1	Sequence 1, Appli
9	1762	50.1	367	σ	US-10-094-168B-3	
7	1366.5	38.9	875	σ	US-10-115-515-23	23,
80	1366.5	38.9	875	σ	US-10-094-168B-5	Sequence 5, Appli
6	1355.5	38.6	875	6	US-10-115-515-10	Sequence 10, Appl
10	1352	38.5	833	10	US-09-891-216-3	
11	926	27.2	789	10	US-09-321-801-2	7
12	926	27.2	791	10	US-09-321-801-4	4,
13	950	27.0	779	10	US-09-420-190-1	1,
14	934.5	26.6	905	12	US-10-094-989-4	Sequence 4, Appli
15	934.5	26.6	920	12	US-10-094-989-2	Sequence 2, Appli
16	934.5	26.6	941	10	US-09-883-825-45	Sequence 45, Appl
17	929	26.4	196	10	US-09-321-801-15	Sequence 15, Appl
18	920.5	26.2	921	10	US-09-883-825-39	Sequence 39, Appl
19	920.5	26.2	921	12	US-10-094-989-5	5, A

Sequence 43, Appl Sequence 2, Appli Sequence 5, Appli Sequence 17, Appl		6 16, 23, 47,	Sequence 10, Appl Sequence 9, Appli Sequence 51, Appl Sequence 6, Appli Sequence 8, Appli Sequence 50, Appli	4, H 2, H 2, H 3, H
10 US-09-883-825-43 9 US-10-202-107-2 10 US-09-891-216-5 10 US-09-891-216-17 9 US-10-083-620A-19	9 US-10-083-620A-21 10 US-09-802-741A-1 9 US-10-083-620A-2 0 US-10-083-620A-17 10 HS-09-801-216-3	ומממ	9 US-10-00/-514-10 9 US-10-067-514-9 9 US-10-076-597-51 9 US-10-067-514-6 9 US-10-067-514-9 9 US-10-076-597-50	9 US-10 067-514-4 9 US-10-067-514-2 0S-10-067-597-46 9 US-09-966-781A-1 9 US-09-966-781A-1 9 US-09-966-781A-1
942 773 142 142 533	580 593 320 34	134 430 712 507	507 585 673 687 745	745 809 647 426 426
26.2 25.6 18.9 12.3	12.0	10.8	10.4 10.4 10.4 10.4 10.4	10.4 10.4 10.3 9.9 9.9
920.5 899 665.5 665.5 431	421 421 420 411 981	381 376 365	364 364 364 364	. 364 362.5 349 347 346
20 21 22 23 24	255 255 26 28	33 33 33 33 33	2 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 3 2 1 2 1 3 2 1 3 3 3 3 3 3 3 3 3 3 3 3

ALIGNMENTS

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Sequence 14, Application US/09891216

Patent No. US2002010312041

GENERAL INFORMATION:

APPLICANT: Ramakrishnan, Shyam

TITLE OF INVENTION: Regulation of Human

TITLE OF INVENTION: Phosphodiesterase-Like Enz

FILE REFERENCE: 02973.00511

CURRENT APPLICATION NUMBER: US/09/891,216

CURRENT FILING DATE: 2001-06-26

PRIOR PAPLICATION NUMBER: US 60/213,998

PRIOR PILING DATE: 2000-06-26

PRIOR FILING DATE: 2001-06-26

PRIOR FILING DATE: 2001-06-26

PRIOR PELICATION NUMBER: PCT/EP01/07289

PRIOR PELICATION NUMBER: PCT/FP01/07289

PRIOR PELING DATE: 2001-06-26

NUMBER OF SEQ ID NOS: 20

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
US-09-891-216-14
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TYPE: PRT
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.; 0 100.0%; Score 3516; DB 10; Length 684; 100.0%; Pred. No. 7.9e-297; Indels Mismatches 0 Query Match 100. Best Local Similarity 100. Matches 684; Conservative

1 MLKQARRPLFRNVLSATQWKKVKITRLVQISGASLAEKQEKHQDFLIQRQTKTKDRRFND 60

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Qy	61 EIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYLPFCGIAI 120	APFTEDDEKVMQMYLPFCGIAI 1	120
qq	61 EIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYLPFCGIAI 120	APFTEDDEKVMQMYLPFCGIAI 1	120
Qy	121 SNAQLEAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCERCSVLLLED 180	KIMHRAQTLLKCERCSVLLLED 1	180
qq	121 SNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCERCSVLLLED 180	KIMHRAQTLLKCERCSVLLLED 1	180

181 IESPVVKFTKSFELMSPKCSADAENSFKESMEKSSYSDWLINNSIAELVASTGLPVNISD 240

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QRLFEAFVIFCGLGINNTIMYDQVKKSWAKQSVALDVLSYHATCSKAEVDKFKAANIPLV 353
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                                                                      SVLLLEDIESPVVKFTKSFELMSPKCSADAENSFKESMEKSSYSDWLINNSIAELVASTG
                                                         LPVNISDAYQDPRFDAEADQISGFHIRSVLCVPIWNSNHQIIGVAQVLNRLDGKPFDDAD
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Pred. No. 1.6e-273;
1; Mismatches 0;
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TITLE OF INVENTION: Regulation of Human
TITLE OF INVENTION: Regulation of Human
TITLE OF INVENTION: Phosphodiesterase-Like Enz
FILE REFERENCE: 02973.00511
CURRENT APPLICATION NUMBER: US/09/891,216
CURRENT APPLICATION NUMBER: US 60/213,998
PRIOR APPLICATION NUMBER: US 60/213,998
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-06-26
PRIOR FILING DATE: 2001-06-26
PRIOR FILING DATE: 2001-06-26
PRIOR SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KWEELHQKRLLASTASSSSPASVMVAKEDRN 684
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99.8%;
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Best Local Similarity
Matches 630; Conserv
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ORGANISM: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFOGRATION:

APPLICANT: Remarkishnan, Shyam

TITLE OF INVENTION: Phosphodiesterase-Like Enz

TITLE OF INVENTION: Phosphodiesterase-Like Enz

FILE REPERENCE: 02973.00511

CURRENT APPLICATION NUMBER: US/09/891,216

CURRENT FILING DATE: 2001-06-26

PRIOR APPLICATION NUMBER: US 60/213,998

PRIOR FILING DATE: 2000-06-26

PRIOR APPLICATION NUMBER: US 60/293,221

PRIOR FILING DATE: 2001-06-25

; PRIOR PILING DATE: 2001-06-26

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                     661 KRLLASTASSSSPASVMVAKEDRN 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 12, Application US/09891216; Patent No. US20020103120A1; GENERAL INFORMATION:
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US-09-891-216-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DQVKKSWAKQSVALDVLSYHATCSKAEVDKFKAANIPLVSELAIDDIHFDDFSLDVDAMI 374
                                                   TAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLYHNWRHAFNVCQLMFAMLTTAG 434
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                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/10094168B
Publication No. US20030092156A1
GENERAL INFORMATION:
APPLICANT: Pinilips, Stephen C.; Harrow, Ian
APPLICANT: Lanfear, Jerry; Fawcett, Lindsay
APPLICANT: Bandama, Olga
TITLE OF INVENTION: ANTIBODES SPECIFICALLY BINDING CYCLIC NUCLEOTIDE PDES
FILE REFERENCE: PF-0623-2 CTP
CURRENT APPLICATION NUMBER: US/10/094,168B
CURRENT APPLICATION NUMBER: US/20/94,168B
PRIOR PILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: US 09/595,514
PRIOR FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PERL PROGram
SSOFTWARE: PERL PROGram
                                                                                                                                                           LQSEGHNIFANLSSKEYSDLMQLLKQSILATDLTLYFERRTEFFELVSKGEYDWNIKNHR
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; OTHER INFORMATION: Incyte ID No. US20030092156A1 HSPDE10A2
US-10-094-168B-3
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                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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Matches 338; Conserv
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181 TAALRWFWELGWVQKFKIDYETLCRWLLTVRKNYRWVLYHNWRHAFNVCQLMPAMLTTAG
                                                             FQDILTEVETLAVIVGCLCHDLDHRGTNNAFQAKSGSALAQLYGTSATLEHHHFNHAVMI
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Drive
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COMPUTER: IBM PC Compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                            301 LQSEGHNIFANLSSKEYSDLMQLLKQSILATDLTLYFEEK 340
                                                                                                                                                  495 LQSEGHNIFANLSSKEYSDLMQLLKQSILATDLTLYFERR 534
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REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/599,658
FILING DATE: 21-Jun-2000
APPLICATION NUMBER: 09/055,584
FILING DATE: 4-JUNE-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/10/115,515
FILING DATE: 03-Apr-2002
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
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STREET: 6300 Sears Tower, 233
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McAllister-Lucas, Lind
Sonnenburg, William K.
Thomas, Melissa K.
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                                                                                                                                                                                                                                                                                                     Sequence 23, Application US/10115515
Publication No. US20030054992A1
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
                                                                                                                                                                                                                                                                                                                                                                                                                      Ferguson, Kenneth M
Francis, Sharron H.
Kadlecek, Ann
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TELEX: 25-3856
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SEQUENCE CHARACTERISTICS
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ZIP: 60606
COMPUTER READABLE FORM:
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STATE: Illinois
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                                                              EDPRFNAEVDQITGYKTQSILCMPIKNHREEVVGVAQAINKKSGNGGTFTEKDEKDFAAY
                                                                                              LPFCG1A1SNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEK1VKK1MHRAQTLLKCER
                                                                                                                                                           CSVLLLEDIESPVVKFTKSFELMSPKCSADAENSFK-----ESMEKSSYSDWL----
                                 KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAIN-KIPEGAPFTEDDEKVMQMY
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S. Wacker I
 Mismatches 186;
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Sonnenburg, William K.
Thomas, Melissa K.
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ADDRESSEE: Marshall, O'Toole,
STREET: 6300 Sears Tower, 233
CITY: Chicago.
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US-10-115-515-10
US-10-115-515-10
Sequence 10, Application US/10115515
Publication No. US20030054992A1
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
Corbin, Jackie D.
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Francis, Sharron H.
Kadlecek, Ann
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 Conservative 129;
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COMPUTER READABLE FORM:
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COUNTRY: USA
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DVLSYHATCSK----AEVDKFKAANIPLVSELAIDDIHFDDFSLDVDAMITAALRMFMELG 385
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APPLICANT: Lanfear, Jerry; Fawcett, Lindsay
APPLICANT: Lanfear, Jerry; Fawcett, Lindsay
APPLICANT: Lanfear, Jerry; Fawcett, Lindsay
TITLE OF INVENTION: ANTHODIES SPECIFICALLY BINDING CYCLIC NUCLEOTIDE PDES
TITLE REPERENCE: PF-0623-2 CIP
CURRENT APPLICATION NUMBER: US/10/094,168B
CURRENT FILING DATE: 2002-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 1999-01-07
PRIOR FILING DATE: 1999-01-07
SOFTWARE: PERL PROGRAM
SOFTWARE: PERL PROGRAM
SOFTWARE: PERL PROGRAM
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                                               LPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCER
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; OTHER INFORMATION: GenBank ID No. US20030092156A1 g3355606
US-10-094-168B-5
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Pred. No. 7.1e-110;
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43.1%;
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Best Local Similarity
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---INNSIAELVASTGLPVNISDAYQDPRFDAEADQISGFH---IRSVLCVPIWN-SNHQ 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DVLSYHATCSK----AEVDKFKAANIPLVSELAIDDIHFDDFSLDVDAMITAALRMFMELG 385
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                                                                                                                                                                                                                                                                                                                                       875;
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                       Version #1.25
                                                                                                                                                                                                                                                                                                                                                            187;
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                                                                                                                                                  NAME: No. US20030054992Aland, Greta
                                                                                                                                                                                                                                                                                                                                     Score 1355.5;
Pred. No. 6.4e-
29; Mismatches
                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/599,658
FILING DATE: 21-Jun-2000
APPLICATION NUMBER: 09/055,584
                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-115-515-10
                                                                                                                                                            REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32706
                                                                                                                                                                                           TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                             FILING DATE: 4-JUNE-1998
                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 875 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 42.9%; Pro
Matches 279; Conservative 129;
                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                INFORMATION FOR SEO ID NO: 10:
                                                                                                                                                                                                                                                                                                                                      38.6%;
42.9%;
                                                                                                                                                                                                                                                                              TOPOLOGY: Linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---KPFDDADQRLFEAFVIFCGLGINNTIMYDQVKKSWAKQSVALDVLSYHATCSKAEVD 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KFK---AANIPLVSELAIDDIHFDDFSLDVDAMITAALRMFMELGMVQKFKIDYETLCRW 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      519
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EDPRFNAEVDQITGYKTQSILCMPIKNHREEVVGVAQAINKKSGNGGTFTEKDEKDFAAY
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  672
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625 SICMPLYQALVKVNVKLKPMLDSVATNRSKWEEL--HQKRLLASTASSSS
                             :||: ||:|| |: ||:|| 813 AICLQLYEALTHVSEDCFFLLDGCRKNRQKWQALAEQOEKTLINGESSOT
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                                                                                                                                                                                                                                                      TITLE OF INVENTION: Regulation of Human
TITLE OF INVENTION: Phosphodiesterase-Like Enzyme
FILE REFERENCE: 0.2973.0651,
CURRENT APPLICATION NUMBER: US/09/891,216
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/213,998
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/293,221
PRIOR PILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: PCT/FE01/07289
PRIOR FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 20
SOFTMARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1352; DB 10;
Pred. No. 1.2e-108;
9: Mismatches 198;
                                                                                                                                                                  Sequence 3, Application US/09891216
Patent No. US20020103120A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative 129;
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                                                                                                                                                                                                                                  APPLICANT: Ramakrishnan, Shyam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               275;
                                                                                                                                         US-09-891-216-3
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241 WASVAIHQVQVCRGLAKQTELNDFLLDVSKTYFDNIVAIDSLLEHIMIYAKNLVNADRCA 300
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643 KQLEEMYQTGSLNLNNQSHRDRVIGLMMTACDLCSVTKPWPVTKLTANDIYAEFWAEGD- 701
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                                  ERLELKLTPSAIFDRNRKDELPRLQLEWIDSICMPLYQALVKVNVKLKPMLDSVATNRSK
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                                                                                                                                                                                                                                                                               APPLICANT: Lanfear, Jeremy
APPLICANT: Robas, Nicola M.
TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES
                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/321,801
CURRENT FILING DATE: 1999-05-27
CURRENT FILING DATE: 1998-12-04
EARLIER FILING DATE: 1998-12-04
EARLIER FILING DATE: 1998-12-04
EARLIER FILING DATE: 1998-12-04
EARLIER FILING DATE: 1998-10-30
EARLIER FILING DATE: 1998-00-09
EARLIER FILING DATE: 1998-04-09
EARLIER APPLICATION NUMBER: 9910801.1
EARLIER FILING DATE: 1998-04-09
EARLIER FILING DATE: 1998-04-09
EARLIER FILING DATE: 1998-04-09
EARLIER FILING DATE: 1998-05-10
NUMBER OF SEQ ID NOS: 19
                                                                                                        WEELHQKRLLASTASSSSPASVMVAKED 682
                                                                                                                            Sequence 4, Application US/09321801
Patent No. US20020115176A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Human
US-09-321-801-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCERCS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LFQVDH------KNKELYSDLFDIGEEKEGKPVFKKTKEIRFSIEKGIAGQVARTGE 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       350 VLNIPDAYADPRFNREVDLYTGYTTRNILCMP1-VSRGSVIGVVQMVNKISGSAFSKTDE 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NWRHAFNVCQLMFAMLTTAGFQDILTEVEILAVIVGCLCHDLDHRGTNNAFQAKSGSALA 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            535 TEFFELVSKGEYDWNIKNHRDIFRSMLMTACDLGAVTKPWEISRQVAELVTSEFFEQGDR 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLLLEDIESPVVKFTKSFELMSPKCSADAENSFKESMEKSSYSDWLINNSIAELVASTGL
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                                                                                                                                                                                 APPLICANT: Lanfear, Jeremy
APPLICANT: Lanfear, Jeremy
APPLICANT: Robas, Nicola M.
FITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES
FILE REFERENCE: PC9477A
CURRENT APPLICATION NUMBER: US/09/321,801
CURRENT APPLICATION NUMBER: 9826777
EARLIER APPLICATION NUMBER: 9828277
EARLIER APPLICATION NUMBER: 98182.7
EARLIER FILING DATE: 1998-10-30
EARLIER FILING DATE: 1998-10-30
EARLIER FILING DATE: 1998-10-30
EARLIER APPLICATION NUMBER: 991820.9
EARLIER APPLICATION NUMBER: 991820.1
EARLIER APPLICATION NUMBER: 991820.1
EARLIER RILING DATE: 1998-05-10
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 2
LENGTH: 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136; Mismatches
                                    |:|| | | | || : | | || || DCLPLLDGCRKNRQKWQALADQQEKTLL 823
                  664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.2%; Score 956; 33.4%; Pred. No. 2
                KLKPMLDSVATNRSKWEEL - - - HQKRLL
                                                                                                                                       Sequence 2, Application US/09321801 Patent No. US20020115176A1
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Best Local Similarity 33.49
Matches 210; Conservative
                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
CRGANISM: Human
US-09-321-801-2
                                                                                                                       US-09-321-801-2
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             644
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                                                                                                                                                                                                                              Sequence 1, Application US/09420190
Patent No. US20020081633A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rapeller-Libermann, Rosana
APPLICANT: Hunter, John Joseph
APPLICANT: Hulliamson, Mark
TITLE OF INVENTION: Methods for Using 22045, A Human Cyclic
TITLE OF INVENTION: Nucleotide Phosphodiesterase
FILE REFERENCE: 5800-71
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                                                                                                                                            WEELHOKRLLASTASSSSPASVMVAKED 682
                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/420,190 CURRENT FILING DATE: 1999-10-18 NUMBER OF SEQ. ID NOS: 2 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ. ID NO 1
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Best Local Similarity
Matches 210; Conserv
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ORGANISM: HOMO
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US-09-420-190-1
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                                                                                                DDEKVMQMYLPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHR 163
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535 TEFFELVSKGEYDWNIKNHRDIFRSMLMTACDLGAVTKPWEISRQVAELVTSEFFEQGDR
                                                                            ERLELKLTPSAIFDRNRKDELPRLQLEWIDSICMPLYQALVKVNVKLKPMLDSVATNRSK
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                                    KQLEEMYQTGSLNLNNQSHRDRVIGLMMTACDLCSVTKLWPVTKLTANDIYAEFWAEGD-
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                                                                                                                                                                                                                                                                                 Sequence 4, Application US/10094989
Patent No. US20020115179A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUM
TITLE OF INVENTION: PROSPHODIESTERASE PROTEINS, AND USES THEREOF
FILE REPERENCE: CLOOLOGABIV
CURRENT APPLICATION NUMBER: US/10/094,989
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 09/754,250
PRIOR FILING DATE: 2001-01-05
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Pred. No. 2.6e-72
l; Mismatches 25:
                                                                                                                                                      WEELHQKRLLASTASSSSPASVMVAKED 682
                                                                                                                                                                            WEKVIRGEETATWISSPSVAQKAAASED 779
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SOFTWARE: FastSEQ for Windows Version 4.0
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33.1%;
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US-10-094-989-4
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Best Local Simil
Matches 212;
                                                                                                                                                                                                                                                     RESULT 14
US-10-094-989-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDDEXTKLLHDGIQPVAAI---DSNFASFTYTPRSLPEDDTSMAILSMLQDMNFINNYKI 613
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                                   572 KPWEISROVAELVTSEFFEQGDRERLELKLTPSAIFDRNRKDELPRLQLEWIDSICMPLY 631
719 QRMLDLMRDIILATDLAHHLRIFKDLQKMAEVG-YDRNNKQHHRLLLCLLMTSCDLSDQT 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                APPLICANT: WEI, Ming-Hui et al TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE TITLE OF INVENTION: ISOLATED HUMAN PROSPINS, NUCLEIC ACID MOLECULES ENCODING HUMAN TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF FILE REFERENCE: CLOO1063DIV CURRENT APPLICATION NUMBER: US/10/094,989 CURRENT FILING DATE: 2002-03-12 PRIOR PAPLICATION NUMBER: 09/754,250 PRIOR FILING DATE: 2001-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 920;
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                                                                                                            632 QALVKVNVKLKPMLDSVATNRSKWEELHQKRLLASTASSSS 672
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SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. US20020115179A1
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US-10-094-989-2
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		Gaps	MSPKCSADAENSFKESMEKSSYSDWLINNSIAELVASTGLPVNISDAYQDPRFDAEADQI 	SGFHIRSVLCVPIWNSNHQIIGVAQVLNRLDGKPFDDADQRLFEAFVIFCGLGINNTIMY	DQVKKSWAKQSVALDVLSYHATCSKAEVDKFKAANIPLVSELAIDDIHFDDFSLDVDAMI 	TAALKMEMELGMVQKEKIDYETLCRWLLTVRKNYRMYLYHNWRHAFNVCQLMFAMLTTAG
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Sequence Seq		490;	10DI	IFCC IFCC	HFDI HFDI	100 100 100 100 100 100 100 100 100 100
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напоменененовочене	ULT 1 09-226-741-1 09-226-741-1 acquence 1, Application US/09226741 actart No. 6100037 ENERAL INFORMATION: APPLICANT: Pillilps, Stephen C. APPLICANT: Endear, Jerry APPLICANT: Landsay APPLICANT: Bandman, Olga CURRENT FILING DATE: 1999-01-07 NUMBER OF SEO ID NOS: 7 SOFTWARE: FastSEQ for Windows Version LEO ID NO 1 LEO ID NO 3 TYPE: PRT OGRANISM: HOMO SAPIENS FEATURE: COTHER INFORMATION: HSPDEIDAL	72.3%; 100.0%; ive	SMEK	SNHO	/LSY LSY	XXID I X I D
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                                              LPRLQLEWIDSICMPLYQALVKVNVKLKPMLDSVATNRSKWEELHQKRLLASTASSSSPA
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Pred. No. 3.2e-231;
0; Mismatches 0;
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APPLICANT: Fawcett, Lindsay
APPLICANT: Bandman, Olga
THE OF INVENTION: HUMAN CYCLIC NUCLEOTIDE
FILE REFERENCE: PF-0623-1 CIP
CURRENT APPLICATION NUMBER: US/09/595,514
                                                                                                                                                                                                                                                                                                                                               FastSEQ for Windows Version 3.0
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PRIOR APPLICATION NUMBER: 09/226,741
PRIOR FILING DATE: 1999-01-07
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100.0%; Pre
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                                                                                                                                                                                                   GENERAL INFORMATION: APPLICANT: Phillips, Stephen C.
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; ORGANISM: HOMO SAPIENS
; , OTHER INFORMATION: HSPDEIOAl
US-09-595-514-1
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Matches 490; Conservative
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SOFTWARE: FastSEQ for
SEQ ID NO 1
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APPLICANT: Lanfear, Jerry
APPLICANT: Lanfear, Jerry
APPLICANT: Eawcett, Lindsay
APPLICANT: Bandman, Olga
TITLE OF INVENTION: HUMAN CYCLIC NUCLEOTIDE PDES
FILE REFERENCE: PF-0623-1 CIP
CURRENT PAPLICATION NUMBER: US/09/595,514
CURRENT FILING DATE: 2000-06-14
PRIOR FILING DATE: 1999-01-07
                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Phillips, Stephen C.
APPLICANT: Phillips, Jefry
APPLICANT: Lindsay
APPLICANT: Bandman, Olga
ITTLE OF INVENTION: HUMAN CYCLIC NUCLEOTIDE PDES
FILE REFERENCE: PP-0623 US
CURRENT APPLICATION NUMBER: US/09/226,741
CURRENT FILIKG DAFE: 1999-01-07
NUMBER OF SEG ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 6.4e-158;
1; Mismatches 1;
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Patent No. 6416991
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99.4%;
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Best Local Similarity 99.49
Matches 338; Conservative
ORGANISM: HOMO SAPIENS
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Francis, Sharron H.
Francis, Sharron H.
Kadlecek, Ann
Loughney, Kate
MCAllister-Lucas, Linda M.
Sonnenburg, William K.
Thomas, Melissa K.
VENTION: Cyclic GMP-Specific
                                                                                                                  Length 367;
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                                                                                                                                               Indels
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                                                                                                                  Score 1762; DB 4;
Pred. No. 6.4e-158;
1; Mismatches 1;
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,547A
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YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23, Application US/08480547A Patent No. 5652131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: No. 5652131and, Greta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beavo, Joseph A.
Corbin, Jackie D.
                                                                                                                  50.1%;
ilarity 99.4%;
Conservative
                                                              ORGANISM: HOMO SAPIENS
COTHER INFORMATION: HSPDE10A2
US-09-595-514-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Sonnenburg, WAPPLICANT: Thomas, MelisTITLE OF INVENTION: CYCLTILE OF INVENTION: PhosNUMBER OF SEQUENCES: 23 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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Best Local Similarity
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STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-480-547A-23
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APPLICANT:
APPLICANT:
APPLICANT:
            SOFTWARE: Fas
SEQ ID NO 3
LENGTH: 367
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                                                                                                                                            Matches 338;
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54 KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAIN-KIPEGAPFTEDDEKVMQMY 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---INNSIAELVASTGLPVNISDAYQDPRFDAEADQISGFH----IRSVLCVPIWN-SNHQ 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            404 ANKINYMYAQYYKNTMEPLNIPDVSKDKRFPWTTENTGNVNQQCIRSLLCTPIKNGKKNK 463
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                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                186;
                                                                                                                                                                                                                                                                                                                 38.9%; Score 1366.5; DB 1
43.1%; Pred. No. 5.5e-120;
                                                                                                                                                                                                                                                                                                                                                           Conservative 129; Mismatches
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APPLICANT: Beavo, Joseph A. APPLICANT: Corbin, Jackie D.
35,302
ER: 32791
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Corbin, Jackie D.
Ferguson, Kenneth M.
Francis, Sharron H.
Kadlecek, Ann
                REFERENCE/DOCKET NUMBER: 32791
TELECOMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 875 amino acids
                                                                                                                                                                                875 amino acids amino acids
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565 CDLGAVTKPWEISRQVAELVTSEFFEQGDRERLELKLTPSAIFDRNRKDELPRLQLEWID 624
                       445 LAVIVGCLCHDLDHRGTNNAFQAKSGSALAQLYGTSATLEHHHFNHAVMILQSEGHNIFA
                                                                                                        505 NLSSKEYSDLMQLLKQSILATDLTLYFERRTEFFELVSKGEYDWNIKNHRDIFRSMLMTA
                                                                                                                                                                                                                                                                                                  625 SICMPLYQALVKVNVKLKPMLDSVATNRSKWEEL--HQKRLLASTASSSS 672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific TITLE OF INVENTION: Phosphodiesterase Materials and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRUT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,949A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 38.9%; Score 1366.5; DB 2; Best Local Similarity 43.1%; Pred. No. 5.5e-120; Matches 280; Conservative 129; Mismatches 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/068,051
FILING DATE: 27-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McAllister-Lucas, Linda
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 23, Application US/08463949A Patent No. 5955583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sonnenburg, William K. Thomas, Melissa K.
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RATION NUMBER: 35,302
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Ferguson, Kenneth M
Francis, Sharron H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Beavo, Joseph A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 27-MAY-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kadlecek, Ann
Loughney, Kate
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INFORMATION FOR SEQ ID NO:
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | | | : | : | | | : | 404 ANKINYMYAQYVKNTMEPLNIPUSUSKENTENTGNVNQQCIRSELCTPIKNGKKNK 463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---INNSIAELVASTGLPVNISDAYQDPRFDAEADQISGFH---IRSVLCVPIWN-SNHQ 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274 IIGVAQVLNRLDG-----KPFDDADQRLFEAFVIFCGLGINNTIMYDQVKKSWAKQSVAL 328
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                                    APPLICANT: Sonnenburg, William K.
APPLICANT: Thomas, Melissa K.
TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific TITLE OF INVENTION: Phosphodiesterase Materials and Methods CORRESPONDENCE: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                3: Marshall, O'Toole, Gerstein, Murray & Borun
6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Matches 280; Conservative 129; Mismatches 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.9%; Score 1366.5; 43.1%; Pred. No. 5.5e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/068,051
FILING DATE: 27-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5702936and, Greea E.
REGISTRATION NUMBER: 35,302
REFENDE/COCKET NUMBER: 32083
TELECOMMUNICATION:
TELEPHONE: (312) 474-6430
                     McAllister-Lucas, Linda M.
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/250,847B
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                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
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INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                               Floppy disk
Loughney, Kate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        875 amino acids
                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
                                                                                                                                                                                                       Chicago
: Illinois
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                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 60606
                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
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                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
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                         LPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCER
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KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAIN-KIPEGAPFTEDDEKVMQMY
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APPLICANT: Francis, Sharron H.
APPLICANT: Kadlecek, Ann
APPLICANT: Loughney, Kate
APPLICANT: Sonnenburg, William K.
APPLICANT: Thomas, Melissa K.
TITLE OF INVENTION: Cyclic GMP-Specific
TITLE OF INVENTION: Phosphodiesterase Materials and Methods
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Patent No. 6037119
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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APPLICANT: Beavo,
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CITY: Chicago
STATE: Illinois
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                                                                                    Version #1.25
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                                                                                                                                                                              US/08/464,410A
SOFTWARE: PATENTE RC-DOS/MS-DOS SOFTWARE: PATENTE Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/464,410A FILING DATE: June 5 1000 CLACOTION.
                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 6037119and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866,
TELECOMMUNICATION INFORMATION:
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TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
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amino acid
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GENERAL INFORMATION:
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                         GENERAL INFORMATION:
APPLICANT: Phillips, Stephen C.
APPLICANT: Lanfear, Jerry
APPLICANT: Lanfear, Jerry
APPLICANT: Bandman, Olga
TITLE OF INVENTION: HUMAN CYCLIC NUCLEOTIDE PDES
FILE REFERENCE: PP-0623 US:
CURRENT APPLICATION NUMBER: US/09/226,741
CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5:
LENGTH: 875
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                                                                                                                                                                                                                                                                                                   Best Local Similarity 43.1%; pred. No. 5.5e-120;
Matches 280; Conservative 129; Mismatches 186;
                                                                                                                                                                                                                                                                                      38.9%; Score 1366.5; 43.1%; Pred. No. 5.5e
Sequence 5, Application US/09226741 Patent No. 6100037
                                                                                                                                                                                                                                                OTHER INFORMATION: GI 3355606
                                                                                                                                                                                                                     ORGANISM: HOMO SAPIENS
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                                                                                                                                        Bandman, Olga
VENTION: HUMAN CYCLIC NUCLEOTIDE PDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1366.5;
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                                                                                                                                             APPLICANT: Bandman, Olga
TITLE OF INVENTION: HUMAN CYCLIC NUCLEON:
FILE REFERENCE PF-0623-1 CIPP.
CURRENT APPLICATION NUMBER: US/09/595,514
CURRENT FILING DATE: 2000-06-14
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1999-01-07
Phillips, Stephen C.
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43.1%;
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                                           Lanfear, Jerry
Fawcett, Lindsay
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PRIOR FILING DATE: 1999-0
NUMBER OF SEQ ID NOS: 7
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LENGTH: 875
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RESULT 11 PCT-US94-06066-23

RESULT 10 US-09-595-514-5 ; Sequence 5, Application US/09595514

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LAVIVGCLCHDLDHRGTNNAFQAKSGSALAQLYGTSATLEHHHFNHAVMILQSEGHNIFA 504
                                                                        565 CDLGAVTKPWEISRQVAELVTSEFFEQGDRERLELKLTPSAIFDRNRKDELPRLQLEWID 624
                                                                                                                                                                                                                                                                                                                            54 KDRRFINDEIDKLTGYKTKSLLCMPIRSSÖGEIIGVAQAIN-KIPEGAPFTEDDEKVMQMY 112
                                                                                                                                                              NLSSKEYSDLMQLLKQSILATDLTLYFERRTEFFELVSKGEYDWNIKNHRDIFRSMLMTA 564
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                                                                                                                                                                                                                                                                                                                                                                                                                     SICMPLYQALVKVNVKLKPMLDSVATNRSKWEEL--HQKRLLASTASSSS 672
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APPLICANT: Thomas, Melissa K.
TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
TITLE OF INVENTION: Phosphodiesterase Materials and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: Marshall, O'Toole, Gerstein, Murray & Borun
6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 38.6%; Score 1355.5; DB 1; Length Best Local Similarity 42.9%; Pred. No. 6e-119; Matches 279; Conservative 129; Mismatches 187; Indels
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ferguson, Kenneth M.
APPLICANT: Francis, Sharron H.
APPLICANT: Kadlecek, Ann
APPLICANT: Loughney, Kate
APPLICANT: MCAllister-Lucas, Linda M.
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5652131and, Greta E.
NAME: NO. 1000 SERVING SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/08480547A Patent No. 5652131 GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 10:
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TYPE: amino acid
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Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 274 IIGVAQVLNRLDG-----KPFDDADQRLFERAFVIFCGLGINNTIMYDQVKKSWAKQSVAL 328
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                                                    APPLICANT: The Board of Regents of the University of Washington TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific TITLE OF INVENTION: Phosphodiesterase Materials and Methods NUMBER OF SEQUENCES: 23 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                        S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 43.1%; Pred. No. 5.5e Matches 280; Conservative 129; Mismatches
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APPLICATION NUMBER: US 08/068,051
FILING DATE: 27-MAY-1993
ATTORNEY/AGENT INFORMATION:
Sequence 23, Application PC/TUS9406066 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                    ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233
                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 320
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                               CITY: Chicago
STATE: Illinois
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE
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APPLICATION NUMBER:
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US-08-463-949A-10
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EDPRFNAEVDQITGYKTQSILCMPIKNHREEVVGVAQAINKKSGNGGTFTEKDEKDFAAY 296
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                                                                                 CSVLLLEDIESPVVKFTKSFELMSPKCSADAENSFK -----ESMEKSSYSDWL----
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APPLICANT: Ferguson, Kenneth M.
APPLICANT: Francis, Sharron H.
APPLICANT: Kadlecek, Ann
APPLICANT: McAllister-Lucas, Linda M.
APPLICANT: McAllister-Lucas, Milliam K.
APPLICANT: Thomas, Melissa K.
TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
TITLE OF INVENTION: Phosphodiesterase Materials and Methods
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Drive
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S. Wacker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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IBM PC compatible
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MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
                                                                                                             CTIFIVDE----
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STREET: boc.
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EDPRFNAEVDQITGYKTQSILCMPIKNHREEVVGVAQAINKKSGNGGTFTEKDEKDFAAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                454 VIGVCQLVNKMEETTGKVKAFNRNDEQFLEAFVIFCGLGIQNTQMYEAVERAMAKQMVTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 386 MVQKFKIDYETLCRWLLTVRKNYRM-VLYHNWRHAFNVCQLMFAMLTTAGFQDILTEVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAVIVGCLCHDLDHRGTNNAFQAKSGSALAQLYGTSATLEHHHFNHAVMILQSEGHNIFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1355.5; DB 1;
Pred. No. 6e-119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative 129; Mismatches 187;
US/08/250,847B
                                                                                                                                                                  No. 5702936and, Greta E. RATION NUMBER: 35,302
                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                    TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.6%;
42.9%;
                                                                                                                                                                                                                                                                     (312) 474-6300
                                                                                                                  FILING DATE: 27-MAY-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          875 amino acids
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                     . TOPOLOGY: linear
MOLECULE TYPE: protein
                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                  NAME: No. 5702936and REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTIFIVDE ----
                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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Matches 279; Conserv
                                             CLASSIFICATION:
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US-08-250-847B-10
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633

504

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574 LVQNFQMKHEVLCKWILSVKNYRKNVAYHNWRHAFNTAQCMFAALKAGKIQKRLTDLEI 633
                                                                                                                                                                                                                                 329 DVLSYHATCSK---AEVDKFKAANIPLVSELAIDDIHFDDFSLDVDAMITAALRMFMELG 385
                                                                                                                 386 MVQKFKIDYETLCRWLLTVRKNYRM-VLYHNWRHAFNVCQLMFAMLTTAGFQDILTEVEI 444
                                                                                                                                                                                                         445 LAVIVGCLCHDLDHRGTNNAFQAKSGSALAQLYGTSATLEHHHFNHAVMILQSEGHNIFA 504
                                                                                                                                                                                                                                                                                                 NLSSKEYSDLMQLLKQSILATDLTLYFERRTEFFELVSKGEYDWNIKNHRDIFRSMLMTA 564
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APPLICANT: Ferguson, Kenneth M.
APPLICANT: Francis, Sharron H.
APPLICANT: Kadlecek, Ann
APPLICANT: Loughney, Kate
APPLICANT: Sonnenburg, William K.
APPLICANT: Thomas, Walissa K.
TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
TITLE OF INVENTION: Phosphodiesterase Materials and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,410A
FILING DATE: June 5, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27866/32705
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 6037119and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
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TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beavo, Joseph A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (312) 474-6300
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 60606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | :|| | :|| | 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 LPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCER 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221 ---INNSIAELVASTGLPVNISDAYQDPRFDAEADQISGFH---IRSVLCVPIWN-SNHQ 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                394 ANRINYMYAQYVKNTMEPLNIPDVSKDKRFPWTNENMGNINQQCIRSLLCTPIKNGKKNK 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 CSVLLLEDIESPVVKFTKSFELMSPKCSADAENSFK-----ESMEKSSYSDWL----
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                                                                                                                                                                                                                       APPLICANT: Sonnenburg, William K.
APPLICANT: Thomas, Melissa K.
TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific TITLE OF INVENTION: Phosphodiesterase Materials and Methods NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS: 23
CORRESPONDENCE ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.6%; Score 1355.5; DB 2; Length ilarity 42.9%; Pred. No. 6e-119; Conservative 129; Mismatches 187; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,949A
                                                                Beavo, Joseph A.
Corbin, Jackle D.
Corbin, Jackle D.
Ferguson, Keneth M.
Francis, Sharron H.
Kadlecek, Ann
Loughney, Kate
MCAllister-Lucas, Linda M.
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APPLICATION NUMBER: US 08/068,051
FILING DATE: 27-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: NO. 595583and, Greta E. REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32706
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PC-DOS/MS-DOS
Sequence 10, Application US/08463949A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: OUCOUNCOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
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INFORMATION FOR SEQ ID NO: 10:
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                         Chicago
: Illinois
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Best Local Similarity
Matches 279; Conserv
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                                                                  APPLICANT
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                                                                                                                                                                                                                                                                                                                         DVLSYHATCSK---AEVDKFKAANIPLVSELAIDDIHFDDFSLDVDAMITAALRMFMELG 385
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                                                                                                         113 LPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCER
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                              Gaps
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                              55;
    Length 875;
Query Match 38.6%; Score 1355.5; DB 3; Length Best Local Similarity 42.9%; Pred. No. 6e-119; Matches 279; Conservative 129; Mismatches 187; Indels
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Minimum DB Maximum DB

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Title: Perfect score:

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Run on:

Scoring table:

Searched:

pHcgs6n cyclic GMP Cyclic-GMP-stimula Human cyclic-GMP-n

Human cGS-PDE cDNA Human cGS-PDE, SEQ Human phosphodiest

Cyclic-GMP stimula Human cGS-PDE amin

Human interferon-a Human cGMP-stimula

ALIGNMENTS

Oda K, 'Michibata

3516 3516 3294.5 3250 3117.5 2970 2541 2458 1762 1762

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Score

Result Š

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Type 11 phosphodiesterases and encoded genes with activity of hydrolyzing cyclic nucleotides, useful for studying intracellular
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AAR66565
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22-DEC-2000; 2000WO-JP09118.
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01-JUN-2000; 2000JP-0163875.
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N-PSDB; AAH46709.
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Copyright (c) 1993
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                                           human and rat type 11 phosphodiesterases (PDE11). These are useful for studying intracellular signal transduction mechanisms, in screening highly selective inhibitors as drugs for treating diseases associated with the enzymes and for the identification or selection of selective inhibitory action against multiple type phosphodiesterases. The present sequence is a protein of the invention.
                                                                                                                                                 MLKQARRPLFRNVLSATQWKKVKITRLVQISGASLAEKQEKHQDFLIQRQTKTKDRRFND
                                                                                                                                                           IESPVVKFTKSFELMSPKCSADAENSFKESMEKSSYSDWLINNSIAELVASTGLPVNISD
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Pred. No. 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cyclic nucleotide phosphodiesterase and its nucleotide sequence useful for treating cardiovascular disorders, sexual dysfunction and screening for drugs to treat associated disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCERCSVLLLED
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                                                                    cavernosum;
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                                                                      corpus
                                               PDEXV; sexual
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                                                                    cardiovascular disease; gastrointestinal disorder; corpo
kidney; liver; skeletal muscle; testis prostate; spleen
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1.3e-304;
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  nucleotide phosphodiesterase PDEXV.
                                               phosphodiesterase;
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                                               nucleotide
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(PFIZ ) PFIZER INC.
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                                                                            EIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYLPFCGIAI 120
                                                                                                                     SNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCERCSVLLLED 180
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                                             241 AYQDPRFDAEADQISGFHIRSVLCVPIWNSNHQIIGVAQVLNRLDGKPFDDADQRLFEAF
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                                   1 MLKQARRPLFRNVLSATQWKKVKITRLVQISGASLAEKQEKHQDFLIQRQTKTKDRRFND
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             Indels
   7.8e-285;
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             13;
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   93.78;
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            Conservative
   Best Local Similarity
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ATLEHHHFNHAVMILQSEGHNIFANLSSKEYSDLMQLLKQSILATDLTLYFERRTEFFEL
                                                                                      VSKGEYDWNIKNHRDIFRSMLMTACDLGAVTKPWEISRQVAELVTSEFFEQGDRERLELK
                                                                                                                               LTPSAIFDRNRKDELPRLQLEWIDSICMPLYQALVKVNVKLKPMLDSVATNRSKWEELHQ
                                  NVCQLMFAMLTTAGFQDILTEVEILAVIVGCLCHDLDHRGTNNAFQAKSGSALAQLYGTS
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Pred. No. 1.2e-280;
1; Mismatches 0;
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99JP-0364866.
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                                                    Yuasa K,
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22-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22; Length 935;
                                                                                                                                                                                                                                                                                                                              transduction;
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95.6%; Pred. No. 7.8e-269;
iive 9; Mismatches 12;
                                                                                                                                                                                                                                                                                                                            phosphodiesterase; PDE11; signal
KWEELHQKRLLASTASSSSPASVMVAKEDRN
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2000JP-0163875.
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selective inhibition
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                                                                                                                                                                                   Human; phosphodiesterase; diabetes; ischemic heart disease; hypertension; nephritis; pancreatitis; ulcer; allergy; asthma; rheumatism; osteoporosis; pain; anxiety; schizophrenia; manic depressive psychosis; Parkinson's disease; dementia; infectious disease; malignant tumour.
ORLFEAFVIFCGLGINNTIMYDQVKKSWAKQSVALDVLSYHATCSKAEVDKFKAANIPLV 603
                                                                                                                                    RTEFFELVSKGEYDWNIKNHRDIFRSMLMTACDLGAVTKPWEISRQVAELVTSEFFEQGD 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes a human polypeptide which has phosphodiesterase activity. The phosphodiesterase polypeptide and polynucleotide are used for the treatment and prevention of diabetes, ischemic heart disease, hypertension, nephritis, pancreatitis, ulcers, allergies, asthma, rheumatism, osteoporosis, pain, anxiety, schizophrenia, manic depressive psychosis, Parkinson's disease, dementia, infectious diseases, and malignant tumours.
                                                                  SELAIDDIHFDDFSLDVDAMITAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLY
                             HNWRHAFNVCQLMFAMLTTAGFQDILTEVEILAVIVGCLCHDLDHRGTNNAFQAKSGSAL
                                                                                              AQLYGTSATLEHHHFNHAVMILQSEGHNIFANLSSKEYSDLMQLLKQSILATDLTLYFER
                                                                                                                                                                          RERLELKLTPSAIFDRNRKDELPRLQLEWIDSICMPLYQALVKVNVKLKPMLDSVATNRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polypeptides with phosphodiesterase activity and DNA for treatment of diabetes, ischemic heart disease, hypertension, nephritis, pancreatitis, ulcers, allergies, asthma
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N-PSDB; AAH78232.
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                                  Gaps
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 576;
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   Length
                              Indels
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 ; DB 22;
5.4e-256;
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Pred. No. 5.46
0; Mismatches
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/note= "catalytic domain"
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100.0%; Pre
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 84.5%;
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                Local Similario,
les 576; Conservative
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Claim 1;
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                                                                                                                                            New human cyclic nucleotide phosphodiesterases, referred as HSPDE100 and HSPDE10A2, useful for treating and preventing cancer and immune
                                                                                                                                                                                                            The present sequence is that of HSPDE10A1, a novel human cyclic nucleotide phosphodiesterase. The amino acid sequence was deduced from an isolated CDNA clone (see AAA49972). The catalytic domain shares 50% identity with HSPDESA1. The invention provides expression vectors, host cells, antibodies, agonists and antaquoists, as well as methods for diagnosing, treating or preventing disorders associated with expression of HSPDE10A1, especially cancer and immune disorders.
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Pred. No. 8e-218;
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                                                                                        Fawcett L,
                                                                                                                                                                                         English.
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100.0%; Pre
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                      2000WO-US00371
                                            99US-0226741
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                                                                                        Lanfear J,
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                                                                PHARM INC
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Best Local Similarity
Matches 490; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phosphodiesterase activity. The phosphodiesterase polypeptide and polynucleotide are used for the treatment and prevention of diabetes, ischemic heart disease, hypertension, nephritis, pancreatitis, ulcers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         allergies, asthma, rheumatism, osteoporosis, pain, anxiety, schizophrenia, manic depressive psychosis, Parkinson's disease, dementia, infectious diseases, and malignant tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                               nephritis; pancreatitis; ulcer; allergy; asthma; rheumatism; osteoporosis; pain; anxiety; schizophrenia; manic depressive Parkinson's disease; dementia; infectious disease; malignant
                                                                                                                               sequence of a human phosphodiesterase polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present sequence encodes a human polypeptide which has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nephritis,
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Pred. No. 1.9e-210;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polypeptides with phosphodiesterase activity and diabetes, ischemic heart disease, hypertension,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kawabata A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pancreatitis, ulcers, allergies, asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80-82; 105pp; Japanese.
AAG67531 standard; Protein; 474 AA
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100.0%; Prr
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                                                                                      (first entry)
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nes 474; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-570769/64.
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                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-MAR-2000;
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301 YSDLMQLLKQSILATDLTLYFERRTEFFELVSKGEYDWNIKNHRDIFRSMLMTACDLGAV 360
                                                                       TKPWEISRQVAELVTSEFFEQGDRERLELKLTPSAIFDRNRKDELPRLQLEWIDSICMPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human cyclic nucleotide phosphodiesterases, referred as HSPDE10A1 HSPDE10A2, useful for treating and preventing cancer and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of HSPDE10A2, a novel human cyclic nucleotide phosphodiesterase. The amino acid sequence was deduced from an isolated cDNA clone (see AAA49973). HSPDE10A2 is a cereminal splice variant of HSPDE10A1 (see AAV55521), being identical between amino acid residues 1-338, but different in the cereminal portion from residue 339 to 367. It shares 40% identity with HSPDE5A1. The invention provides expression vectors, host cells, antibodies, agonists and antagonists, as well as methods for diagnosing, treating or preventing disorders associated disorders.
                                                                                                                                                                        YQALVKVNVKLKPMLDSVATNRSKWEELHQKRLLASTASSSSPASVMVAKEDRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleotide phosphodiesterase; HSPDE10A2; human; cancer; disorder; diagnosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Harrow I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "phosphodiesterase signature motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "putative cGMP binding motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cyclic nucleotide phosphodiesterase HSPDE10A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1762; DB 21;
Pred. No. 1.7e-148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
88..99
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99.48;
                                                                                                                                                                                                                                                                                                                  AAY95522 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-452539/39.
N-PSDB; AAA49973.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000~\rm or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and .
                                                                                181 TAALRMEMELGMVQKFKIDYETLCRMLLTVRKNYRMVLYHNWRHAFNVCQLMFAMLTTAG 240
                                                                                                                                                                                                               434
                                                                                                                                                                                              FQDILTEVEILAVIVGCLCHDLDHRGTNNAFQAKSGSALAQLYGTSATLEHHHFNHAVMI 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB7737-ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
               TAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLYHNWRHAFNVCQLMFAMLTTAG
SGFHIRSVLCVPIWNSNHQIIGVAQVLNRLDGKPFDDADQRLFEAFVIFCGLGINNTIMY
                                                               DQVKKSWAKQSVALDVLSYHATCSKAEVDKFKAANIPLVSELAIDDIHFDDFSLDVDAMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 42399; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                              LOSEGHNIFANLSSKEYSDLMQLLKQSILATDLTLYFEEK 340
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                                                                                                                                                                                                                                                                                                                                                                             ABB71869 standard; Protein; 1284
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-656860/75.
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                                                                                                                                                                                                                                                    ------KAANIPLVSELAIDDIHFDDFSLDVDAMITAALRMFMELGMVQKFKIDYET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antianaemic; cancer;
                                                KTKDRRFNDEI
                                                                   KKCLVSKLFDVCPRSTVEEMEQQDEVRVAWGTGIAGHVAESGEPVNIPDAYQDERFNCEI
                                                                                            DKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYLPFCGIAISN
                                                                                                                                         AQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCERCSVLLLEDIE
                                                                                                                                                                                        SPVVKFTKSFELMSPKCSADAENSFKESMEKSSYSÖWLINNSIAELVASTGLPVNISDAY
                                                                                                                                                                                                             KG--SFSRVFDFEANDLSEEEATSRTSPYE----SRFPINIGITGHVATTGETVNVPNAY
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                        51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             enzyme; fruitfly; cytostatic; antianaemic;
renal disease; sensory neuropathy; uraemia.
                         Indels
                                                                                                                                                                                                                                                                                   FCGLGINNTIMYDQVKKSWAKQSVALDVLSYHATCSKAEVDKF--
  22;
Score 1511.5; DB 22
Pred. No. 2.5e-125;
5; Mismatches 202;
                        Conservative 126; Mismatches
                                               KKVKITRLVQISGASLAEKQEKHQDFLIQRQT-
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 43.0%;
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            11 Similarity 303; Conserv
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 Query Match
Best Local Si
Matches 303;
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The invention relates to an isolated transketolase-like enzyme be polypeptide. The activity of the polypeptide of the invention may be described as cytostatic and antianaemic. Polypeptides and polynucleotides of the invention can be used to identify agents that modulate the
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                                                                                                                                                                                                                                                                                                                                                                     Novel isolated human transketolase-like enzyme polypeptide, useful for treating cancer, anaemia, end-stage renal disease and sensory neuropathy associated with uraemia .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transkelotase-like enzyme encoding sequence. Fusion proteins including the polypeptide of the invention may be useful in the generation of manibodies and in various assay systems. The current sequence represents the D. melanogaster CG10231 gene product that was used to aid the identification of human transkelotase-like enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activity of a transketolase-like enzyme. They are also useful for treating transketolase-like enzyme disorder such as cancer, anaemia, end-stage renal disease and sensory neuropathy associated with uraemia. Therapeutic agents of the invention are useful for modulating the activity of transketolase-like enzyme in the above mentioned diseases. Polypeptides and polynucleotides os the invention are useful for identifying test compounds which act as agonists or antagonists, for
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three-hybrid assay. They are also useful in diagnostic assays for
detecting diseases and abnormalities or susceptibility to disease and
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30-MAY-2001; 2001WO-EP06125.
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Drosophila melanogaster polypeptide SEQ ID NO 17847.  Drosophila melanogaster polypeptide SEQ ID NO 17847.  Drosophila melanogaster,  Drosophila melanogaster.  WOSODITIO42-A2.  27-SEP-2001.  23-MAR-2000; 2000US-050131.  23-MAR-2000; 2000US-0519157P.  11-JUL-2000; 2000US-0519157P.  WPT: ZOOII-655866077S.  WPT: ZOOII-65586077S.  PRESULT  Disclosure; SEQ ID NO 17847; 21pp + Sequence Listing; English.  Disclosure; SEQ ID NO 17847; 21pp + Sequence Listing; English.  Disclosure; SEQ ID NO 17847; 21pp + Sequence Listing; English.  Disclosure; SEQ ID NO 17847; 21pp + Sequence Listing; English.  Disclosure; SEQ ID NO 17847; 21pp + Sequence Listing; English.  Disclosure; SEQ ID NO 17847; 21pp + Sequence Listing; English.  Disclosure; SEQ ID NO 17847; 21pp + Sequence Listing; English.  Disclosure; SEQ ID NO 17847; 21pp + Sequence Listing; English.  Disclosure; SEQ ID NO 17847; 21pp + Sequence Listing; English.  Disclosure; SEQ ID NO 17847; 21pp + Sequence Listing; English.  Disclosure; SEQ ID NO 17847; 21pp + Sequence Listing; English.  Disclosure; SEQ ID NO 17847; 21pp + Sequence Listing; English.  Disclosure; SEQ ID NO 17847; 21pp + Sequence Listing; English.  Disclosure; SEQ ID NO 17847; 21pp + Sequence Listing; English.  Disclosure; SEQ ID NO 17847; 21pp + Sequence Listing; English.  Disclosure; SEQ ID NO 17847; 21pp + Sequence Listing; English.  Disclosure; SEQ ID NO 17847; 21pp +		63685;	qa	612
Drosophila melanogaster polypeptide SEQ ID NO 17847.  Drosophila; developmental biology; cell signalling; insecticide;  pharmaceutical.  Drosophila melanogaster.  WO200171042-A2.  27-SEP-2001.  23-WAR-2000; 2000US-191637P.  23-WAR-2000; 2000US-191637P.  23-WAR-2000; 2000US-191637P.  23-WAR-2000; 2000US-191637P.  Drosophila melanogaster.  WPI: X001-656860775.  WPI: X001-656860775.  WPI: X001-656860775.  WPI: X001-656860775.  WPI: X001-656860775.  WPI: SEQ ID NO 17847; 21pp + Sequence Listing; English.  Disclosure; SEQ ID NO 17847; 21pp + Sequence Listing; English.  Disclosure; SEQ ID NO 17847; 21pp + Sequence Listing; English.  The invention relates to an isolated nucleic acid detection reagent of acettion is underly and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of the development of acettions in higher eukaryotes for the development of the encoded proteins specification, but was obtained in electronic format discussed DNA acettions the was obtained in electronic format discussed DNA active to the princed at for the part of the princed with the princed at fight without high acetting and accetting and accettin		(first	٥y	3
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Drosophila melanogaster.  WO200171042-A2. 27-SEP-2001. 23-MAR-2001; 2001W0-US09231. 23-MAR-20001; 2000US-191637P. 11-UU-20002; 2000US-191637P. 11-UU-20002; 2000US-191637P. 11-UU-20002; 2000US-191637P. 11-UU-20002; 2000US-191637P. 11-UU-20002; 2000US-191637P. 11-UU-20003; 2000US-19163P. 11-UU-2003; 2000US-19163P. 11-UU-20003; 2000US-19163P. 11-UU-20003; 2000US-19163P. 11-UU-20003; 2000US-19163P. 11-UU-20003; 2000US-19163P. 11-UU-20003; 2000US-19163P. 11-UU-20003; 2000US-19163P. 11-UU-2		developmental biology; cell	QY	4
27-SEP-2001. 23-WAR-2001; 2001WO-US09231. 23-WAR-2001; 2001WO-US09231. 23-WAR-2000; 2000US-191637P. 11-JUL-2000; 2000US-19163P. 11-JUL-2000; 2000US-1		sophila melanogaster.	qq ·	732
27-SEP-2001. 23-MAR-2001; 2001WO-US09231. 23-MAR-2000; 2000US-191637P. 11-JUL_2000; 2000US-191637P. 11-JUL_2000; 2000US-0614150. (PEKE ) PE CORP NY.  Wenter JC, Adams M, Li PWD, Myers EW; WPI; 2001-656860/75. N-PSDB; ABLO7788.  N-PSDB; ABLO7788.  N-PSDB; ABLO7788.  Disclosure; SEQ ID NO 17847; 21pp + Sequence Listing; English.  The invention relates to an isolated nucleic acid detection reagent interactions - the invention is made in elucidating cell signalling and cell-cell interactions in injerse for more gones from Drosophila. The invention is AAY841 cell-cell interactions in higher enkaryotes for the development of more genes from brosophila. The invention is AAY841 cell-cell interactions in higher enkaryotes for the development of more genes from brosophila. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA (ABB37737-ABB72072).  The sequence data for this partent did not form part of the printed specification, but was obtained in electronic format directly from WIPO KW at Itp.Wipo.int/pub/published_pct_sequences.  Sequence 1232 AA;  Sequence 1232 AA;  Sequence 1232 AA;  Sequence 1232 AA;		00171042-A2.	QY	47
23-MAR-2001; 2001WO-US09231.  23-MAR-2000; 2000US-0514150.  11-JUL-2000; 2000US-0514150.  (PEKE ) PE CORP NY.  WPI: 2001-656860/75.  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions.  Disclosure; SEQ ID NO 17847; 21pp + Sequence Listing; English.  Disclosure; SEQ ID NO 17847; 21pp + Sequence Listing; English.  The invention relates to an isolated nucleic acid detection reagent acceptable of detections and pharmaceutical drugs. The invention is No 17847; 21pp + Sequence Call-cell interactions in higher ewkaryotes for the development of acceptable of detections in higher ewkaryotes for the development of acceptable of detections in higher ewkaryotes for the development of sequences (ABL01840-ABL16175) and the encoded proteins  (ABB57737-ABB72072).  The sequence data for this patent did not form part of the printed KWW specification, but was obtained in electronic format directly from WIPO KWW at fftp. Wipo.int/pub/published_pct_sequences.		SEP-2001.	qq	792
11-JUL-2000; 2000US-191637P.  11-JUL-2000; 2000US-0614150.  (PEKE ) PE CORP NY.  Venter JC, Adams M, Li PWD, Myers EW;  WPI; 2001-656860/75.  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell  Disclosure; SEQ ID NO 17847; 21pp + Sequence Listing; English.  The invention relates to an isolated nucleic acid detection reagent and elucidating cell signalling and acid detecting loon or more genes from Drosophila. The invention is AXY84; and in elucidating cell signalling and AC cell-cell interactions in higher eukaryotes for the development of for the development of for the development of format did not form part of the printed acid acts of ABL51737-ABB7202).  The sequences (ABL51675) and the encoded proteins accounted at a for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence acid acid by the sequences.  The sequence acid to this patent did not form part of the printed sequence acid to the printed acid to the printed acid the with the sequences.  The sequence acid to this patent did not form part of the printed sequence acid to the printed acid the with the sequences.			QY	491
Venter JC, Adams M, Li PWD, Myers EW;  WPI; 2001-656860/75.  N-PSDB; ABL07788.  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell bhitteractions.  Disclosure; SEQ ID NO 17847; 21pp + Sequence Listing; English.  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is XX useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of in Sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequence data for this patent did not form part of the printed KWW Specification, but was obtained in electronic format directly from WIPPO KWW Squence 1232 AAA;  Sequence 1232 AAA;			qa o	851
Wenter JC, Adams M, Li PWD, Myers EW;  WPI: 2001-656860/75.  N-PSDB; ABL07788.  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell biteractions.  Disclosure; SEQ ID NO 17847; 21pp + Sequence Listing; English.  Disclosure; SEQ ID NO 17847; 21pp + Sequence Listing; English.  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is XX useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmacutical drugs. The invention discloses genomic DNA sequences (ABL01800-ABL16176) and the encoded proteins (ABL01800-ABL16175) and the encoded proteins (ABB01800-ABL16175) and the encoded pro		) PE	qa	911
WPI; 2001-656860/75.  N-PSDB; ABL07788.  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell Db interactions -  Disclosure; SEQ ID NO 17847; 21pp + Sequence Listing; English.  Disclosure; SEQ ID NO 17847; 21pp + Sequence Listing; English.  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is XX useful in developmental biology and in elucidating cell signalling and capable of detecting and in elucidating cell signalling and discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequence data for this patent did not form part of the printed KW KW specification, but was obtained in electronic format directly from WIPO KW KW Sequence 1232 AA;  KW Sequence 1232 AA;		JC, Adams M, Li PWD,	QY	554
New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell binteractions.  Disclosure; SEQ ID NO 17847; 21pp + Sequence Listing; English.  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is XX useful in developmental biology and in elucidating cell signalling and AC cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA Sequences (ABL16175) and the encoded proteins (ABB77137-ABB72072).  The sequence data for this patent did not form part of the printed KW KW specification, but was obtained in electronic format directly from WIPO KW at fip.wipo.int/pub/published_pct_sequences.		; 2001-656860/75. SDB; ABL07788.	qq	6
Disclosure; SEQ ID NO 17847; 21pp + Sequence Listing; English.  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is XX useful in developmental biology and in elucidating cell signalling and AC cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL016176-ABL3051), expressed DNA Sequences (ABL01800-ABL16176) and the encoded proteins  (ABB57737-ABB572072).  The sequence data for this patent did not form part of the printed KW KW specification, but was obtained in electronic format directly from WIPO KW KW Sequence 1232 AA;		c acid detection reagent for detecting 100 la and for elucidating cell signalling and	do do	10
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is XX useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of DYX insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57377-ABB72072).  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO KW at ftp.wipo.int/pub/published_pct_sequences.			RESI	JLT 13
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insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins sequences (ABL01840-ABL16175) and the encoded proteins (ABB57377-ABB72072).  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO KW at ftp.wipo.int/pub/published_pct_sequences.			XX	AAY848
sequences (ABL01840-ABL16175) and the encoded proteins (ABB777-ABB72072).  XX The Sequence data for this patent did not form part of the printed Specification, but was obtained in electronic format directly from WIPO  XK  XK  XK  XK  Sequence 1232 AA;  KW  KW  KW  KW		ecticides, therapeutics and pharmaceutical drugs. The invention closes genomic DNA sequences (ABLIG176-ABL30511), expressed DNA	Y L X	21-AUG-200
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		uence 1232 AA;	KW	chroni pelvos

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Ouery Match 39.3%; Score 1380.5; DB 22; Length 1232; Best Local Similarity 38.9%; Pred. No. 1.1e-113; Matches 299; Conservative 109; Mismatches 211; Indels 149; Gaps

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EEQTDLEKIVKKIMHRAQTLLKCERCSVLLLE------DIESP-----VVKFTK 190
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EEQNNLECLVTKIMTEARELLKCERCSVFLVDLDCCEASHLEKIIEKPNQPATRAIKSAD 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cyclic GMP; DDE3; DDE5; DDE4 plice variant; DDE4D; cyclic GMP; DDE3; DDE5; DDE4 plice variant; DDE4D; chromic bronchial hyper-reactivity; joint disorder; rheumatoid arthritis; pelvospondylitis; bowel disease; ulcerative colitis; Crohn's disease; autoimmune disease; diabetes mellitus type I; Hashimoto's thyroiditis; systemic lupus erythromacosus; myasthenia gravis; Grave's disease; immune thrombocytopenic purpura; acute respiratory distress syndrome; septic shock; depression; DDE1; DDE2; PDE6; PDE9; PDE10; jet lag;
                                                                                                                                                 VIEWVRDHNQIRAEDEIDS----TQAILCMPIMNAQKKVIGVAQLINKANGVPFTDSDA 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           || | |::|:|||||;:|
ILY-TTSTMEHHHFDHFRLAAFLDRLAAFRRALRDLARELLDLVEELVVDPTLIFLVIEY 850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYNLYSFTFTDFELYDDDTCRAVLRMFMQCNLVSQFQIPYDVLCRWVLSVRKNYRPVKYH 731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RLFEAFVIFCGLGINNTIMYDQVKKSWAKQSVALDVLSYHATCSKAEVDKFKAANIPLVS 354
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87
                                 A----YQDPRFDAEADQISGFHIRSVLCVPIWNSNHQIIGVAQVLNRLDGKPFDDADQ
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VQISCASLAEKQEKHQDFLIQRQTKTKDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIG
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643
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                                                                                                                                                                        DVLSYHATCSK---AEVDKFKAANIPLVSELAIDDIHFDDFSLDVDAMITAALRMFMELG 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            625 SICMPLYQALVKVNVKLKPMLDSVATNRSKWEEL--HQKRLLASTASSSS------ 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phosphodiesterase V; human; hypertension; pulmonary hypertension; atherosclerosis, cerebral infarction; allergic rhinitis; kidney failure; diabetic complication; glaucoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New phosphodiesterase V useful for screening potential phosphodiesterase inhibitors for treatment of hypertensive and allergic diseases.
  221 ---INNSIAELVASTGLPVNISDAYQDPRFDAEADQISGFH---IRSVLCVPIWN-SNHQ
                            404 ANKINYMYAQYVKNTMEPLNIPDVSKDKRFPWTTENTGNVNQQCIRSLLCTPIKNGKKNK
                                                                                                            EVLSYHASAAEEETRELQSLAAAVVPSAQTLKITDFSFSDFELSDLETALCTIRMFTDLN
                                                                                                                                                                                                                                                                                   LAVIVGCLCHDLDHRGTNNAFQAKSGSALAQLYGTSATLEHHHFNHAVMILQSEGHNIFA
                                                                                                                                                                                                                                                           MVQKFKIDYETLCRWLLTVRKNYRM-VLYHNWRHAFNVCQLMFAMLTTAGFQDILTEVEI
                                                                                                                                                                                                                                                                                                                                                                                                                               505 NLSSKEYSDLMQLLKQSILATDLTLYFERRTEFFELVSKGEYDWNIKNHRDIFRSMLMTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDLGAVTKPWEISRQVAELVTSEFFEQGDRERLELKLTPSAIFDRNRKDELPRLQLEWID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human phosphodiesterase V amino acid sequence #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY78940 standard; Protein; 832 AA.
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883 PPVATMVSK 891
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16-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The specification describes a method for modulating the specific effectiveness of I-kappaB kinases or cyclic nucleotide phosphodiesterases which have the ability to cleave cyclic AMP and/or GMP. This involves modulating the specific effectiveness of the cyclic nucleotide phosphodiesterase or I-kappaB kinase by modulating the spatial distribution within cells of the animal. If the cyclic nucleotide phosphodiesterase used is a PDE3, PDE3, PDE8 or a splice variant of PDE4 (such as PDE4D), the method is used to treat inflammatory diseases such as achonic inflammation (especially airway diseases such as achonic bronchial hyper-reactivity of non-asthma etiology, both disorders such as rheumatoid arthritis and pelvospondylitis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAIN-KIPEGAPFTEDDEKVMQMY 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 LPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCER 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bowel diseases such as ulcerative colitis and Crohn's disease, autoimmune diseases associated with inflammation (such as diabetes mellitus type I. systemic lupus erythromatosus, myasthenia gravis, Hashimoto's thyroiditis, Grave's disease and immune thromboyupoenic purpura), disregulations of the immune system (such as acute respiratory distress syndrome (ARDS) and septic shock) and/or depression. Alternatively, if the cyclic nucleotide phosphodiesterase is PDEI, PDE2, PDE6, PDE9, PDE10 or a splice variant of PDE5, the method is used to treat hypo- or hypertension, erectile dysfunction, circadian rhythm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modulating the activity of I-kappaB kinases or cyclic nucleotide phosphodiesterases for the treatment of inflammatory disorders, autoimmune disorders (e.g. diabetes and Crohn's disease) and depression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    resetting or jet-lag. The present sequence represents a fusion protein PDE5D and green fluorescent protein (GFP), which is used in the course
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erectile dysfunction; circadian rhythm;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Page 103-105; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                             Scudder KM,
                    green fluorescent protein; GFP.
PDE5 splice variant; tension;
                                                                                                                                                                                                                                                                                                   98DK-0001322.
98DK-0001323.
                                                                                                                                                                                                                                                                             98DK-0001321
                                                                                                                                                                                                                                    99WO-DK00567
                                                                                                                                                                                                                                                                                                                                                                                                             Terry BR,
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                                                                                                                                                                                                                                                                                                                                                                   (BIOI-) BIOIMAGE AS
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1126 AA;
                                                                                                        Aequorea victoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:: ::::
CTIFIVDE-
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                                                                                                                                                WO200023091-A2.
                                                                                                                                                                                                                                                                                                                                                                                                           Arkhammar POG,
                                                                                      Homo sapiens.
                                                                                                                                                                                                                                  15-OCT-1999;
                                                                                                                                                                                                                                                                                                                       15-OCT-1998;
                                                                                                                                                                                                                                                                               15-0CT-1998
                                                                                                                                                                                        27-APR-2000
                                                                                                                                                                                                                                                                                                     .5-OCT-1998
                                                                Synthetic.
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WPI; 2000-353412/31
                                                                                                                                                                                                                                                                                                                    833 AA;
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                              JP2000095759-A
             sapiens
                                                                        19-JUL-1999;
                                                                                                                                                                 Tricyclic cc
inhibitory a
                                                    04-APR-2000
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                                                                                                                                                                                                                                                              CTIFIVDE-----SDTLTREHD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDLGAVTKPWEISRQVAELVTSEFFEQGDRERLELKLTPSAIFDRNRKDELPRLQLEWID
                                                                                                                                                                                                             ---INNSIAELVASTGLPVNISDAYQDPRFDAEADQISGFH---IRSVLCVPIWN-SNHQ
                                                                                                                                                                                                                                                                                                362 ANKINYMYAQYVKNTMEPLNIPDVSKDKRFPWTTENTGNVNQQCIRSLLCTPIKNGKKNK
                                                                                                                                                                                                                                                                                                                            IIGVAQVLNRLDG-----KPFDDADQRLFEAFVIFCGLGINNTIMYDQVKKSWAKQSVAL
                                                                                                                                                                                                                                                                                                                                                                                                              MVQKFKIDYETLCRWLLTVRKNYRM-VLYHNWRHAFNVCQLMFAMLTTAGFQDILTEVEI
                                                                                                                                                                                                                                                                                                                                                                                                                           KDRRFNDEIDKLIGYKTKSLLCMPIRSSDGEIIGVAQAIN-KIPEGAPFTEDDEKVMQMY
                                                                                                                                                                             EDPRFNAEVDQITGYKTQSILCMPIKNHREEVVGVAQAINKKSGNGGTFTEKDEKDFAAY
                                                                                                                                                                                                  LPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCER
                                                                                                                                                                                                                                          CSVLLLEDIESPVVKFTKSFELMSPKCSADAENSFK-----ESMEKSSYSDWL----
                                                                                                                                     Gaps
                   This sequence represents a human phosphodiesterase V amino acid sequence phosphodiesterase V protein, its fragments and salts are useful the identification of phosphodiesterase V inhibitors for use in the
                                                  treatment of hypertension, pulmonary hypertension, atherosclerosis, cerebral infarction, allergic rhinitis, kidney failure, diabetic complications, and glaucoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cGMP phosphodiesterase V; inhibitor; tricyclic compound; cyclic GMP phosphodiesterase inhibitor; erectile failure; feminine function failure.
                                                                                                                                     55;
                                                                                                                Length 832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SICMPLYQALVKVNVKLKPMLDSVATNRSKWEEL - - HQKRLLASTASSSS
                                                                                                                                     Indels
                                                                                                                DB 21;
                                                                                                                Query Match 38.9%; Score 1366.5; DB 21 Best Local Similarity 43.1%; Pred. No. 1.1e-112; Matches 280; Conservative 129; Mismatches 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cGMP phosphodiesterase V SEQ ID NO:1.
Claim 7; Page 88-90; 96pp; Japanese.
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LALLIAALSHDLDHRGVNNSYIQRSEHPLAQLY-CHSIMEHHHFDQCLMILNSPGNQILS
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EDPRFNAEVDQITGYKTQSILCMPIKNHREEVVGVAQAINKKSGNGGTFTEKDEKDFAAY
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ention of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphodiesterase inhibitors comprising tricyclic compounds or theisalts. The inhibitors are useful for the treatment and prevention exectile failure and feminine function failure. The compounds have excellent CGMP-phosphodiesterase inhibitory action. The present sequence represents human CGMP phosphodiesterase inhibitory action. The present an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CSVLLLEDIESPVVKFTKSFELMSPKCSADAENSFK-----ESMEKSSYSDWL---
                                                                                                                                                                                                                                                                                                      compounds having cyclic GMP-specific phosphodiesterase / action useful as pharmaceuticals, and preparation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 833;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 117; Page 66-68; 71pp; Japanese
99JP-0204103
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Search completed: June 13, 2003, 15:47:18 Job time : 62.4282 secs

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Sequence 2, A
Sequence 4, A
Sequence 15,
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Sequence 15,
Sequence 5,
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                                                                          June 13, 2003, 15:49:06 ; Search time 13.9203 Seconds
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-891-216-15
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US-09-891-216-16
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US-10-115-515-13
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US-09-321-801-2
US-09-321-801-4
US-09-321-801-15
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Maximum Match 100%
Listing first 45 summaries
                                                 OM protein - protein search, using sw model
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1 MLKQARRPLFRNVLSATQWK....
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Sequence 909, App
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Sequence 371, Appl
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Sequence 33, Appl
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                   Sequence 45,
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2.05-10-094-999-5
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0.05-09-383-601-301-464A-909
0.05-09-884-761-40569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/09891216
Patent No. US20020103120A1
GENERAL INFORMATION
APPLICAMY: Ramakishnan, Shyam
TITLE OF INVENTION: Regulation of Human
TITLE OF INVENTION: Regulation of Human
FILER REFERENCE: 02973.0051
CURRENT APPLICATION NUMBER: US/09/891,216
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/213,998
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/293,221
PRIOR APPLICATION NUMBER: US 60/293,221
PRIOR PILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: PCT/FP01/07289
PRIOR FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 20
SOFTWARE FEASTSEQ for Windows Version 4.0
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US-10-033-326-7
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181 IESPVVKFTKSFEL 194

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Sequence 4, Appl:

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Gaps

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PFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC 1,73
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Pred. No. 4.2e-60;
3; Mismatches 3;
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APPLICANT: Ramakrishnan, Shyam
TITLE OF INVENTION: Regulation of Human
TITLE OF INVENTION: Phosphodiesterase-Like Enzyme
FILE REFERENCE: 02973.00511
CURRENT APPLICATION NUMBER: US/09/891,216
CURRENT FILING DATE: 2001-06-26
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TITLE OF INVENTION: Regulation of Human
TITLE OF INVENTION: Phosphodiesterase-Like Enz
TITLE OF INVENTION: Phosphodiesterase-Like Enz
TITLE OF INVENTION: Phosphodiesterase-Like Enz
FILE REFERENCE: 02973.00511
CURRENT APPLICATION NUMBER: US/09/891,216
PRIOR APPLICATION NUMBER: US 60/213,998
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/293,221
PRIOR PLING DATE: 2001-05-25
  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2000-06-26
PRIOR PELICATION NUMBER: US 60/293,221
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: PCT/FEP01/07289
PRIOR FILING DATE: 2001-06-26
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Patent No. US20020103120A1
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95.0%;
  140; Conservative
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Best Local Similarity 95.0
Matches 133; Conservative
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US-09-891-216-5
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                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Ramakrishnan, Shyam
TITLE OF INVENTION: Regulation of Human
TITLE OF INVENTION: Phosphodiesterase-Like Enzyme
FILE REFERENCE: 02973.00511
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APPLICANT: Ramakrishnan, Shyam
TITLE OF INVENTION: Regulation of Human
TITLE OF INVENTION: Phosphodiesterase-Like Enzyme
FILE REFERENCE: 02973,00511
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Pred. No. 2.1e-63;
1; Mismatches 0;
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No. 2.1e-63;
                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/891,216
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/213,998
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-06-25
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FASLESQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 934
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CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/213,998
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
SSOFTWARE: FastSEQ for Windows Version 4.0
SSOFTWARE: PastSEQ for Windows Version 4.0
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                                                                                                                   Sequence 12, Application US/09891216
Patent No. US20020103120A1
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99.3%;
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99.3%;
Query Match
Best Local Similarity 99.3 Matches 140; Conservative
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; ORGANISM: Homo sapiens
US-09-891-216-12
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US-09-891-216-15
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Best Local Similarity
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APPLICANT: Ramakrishnan, Shyam
TITLE OF INVENTION: Regulation of Human
TITLE OF INVENTION: Phosphodiesterase-Like Enzyme
FILE REFERENCE: 02973.00511
CURRENT APPLICATION NUMBER: US/09/891,216
CURRENT PILING DATE: 2001-06-26
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2001-06-26
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
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Pred. No. 8.3e-31;
3; Mismatches 4;
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Pred. No. 8.3e-31;
3; Mismatches 4;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 134
                                                                                                                                                                   NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 134
  CURRENT APPLICATION NUMBER: US/09/891,216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: VARIANT
; LOCATION: (1)...(134)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-891-216-16
                   CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/213, 998
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/293, 221
PRIOR FILING DATE: 2001-05-25
PRIOR PLING DATE: 2001-05-25
PRIOR PLING DATE: 2001-06-26
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COTHER INFORMATION: Xaa = Any Amino Acid
US-09-891-216-2
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Patent No. US20020103120A1
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68.9%;
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Best Local Similarity 68.9%;
Matches 82; Conservative
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Best Local Similarity 68.9<sup>5</sup>
Matches 82; Conservative
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                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                       NAME/KEY: VARIANT
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                                                                                                                                                                                                                                                         PRT
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                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                         TYPE:
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                                                                                                                                                                                                                                                                                                                                                            FCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCERCS 174
                                                                                                                                                                                                                                                                                                                                                                                  1 DRRFNDEIDKLIGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYLP 60
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; Sequence 13, Application US/09891216
; Patent No. US20020103120A1
; GENERAL INFORMATION:
    APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: Phosphodiesterase-Like Enzyme
; TITLE OF INVENTION: Phosphodiesterase-Like Enzyme
; FILE OF INVENTION: Phosphodiesterase-Like Enzyme
; CURRENT APPLICATION NUMBER: US 60/293,231
; PRIOR FILING DATE: 2001-06-26
; PRIOR FILING DATE: 2001-06-26
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1: 576
                                                                                                                                                                                         DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09891216
Patent No. US20020103120A1
GENERAL INFORMATION:
APPLICANT: Ramakrishnan, Shyam
TITLE OF INVENTION: Regulation of Human
TITLE OF INVENTION: Phosphodiesterase-Like Enzyme
FILE REFERENCE: 02973,00511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 429; DB 10;
Pred. No. 3.1e-35;
0; Mismatches 0;
                                                                                                                                                                                       Score 665.5; DB 1 Pred. No. 4.2e-60;
                                                                                                                                                                                                                                 3; Mismatches
                   NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169 KCERCSVLLLEDIESPVVKFTKSFEL 194
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                                                                                                                                                                                         68.3%;
95.0%;
PRIOR FILING DATE: 2001-06-26
                                                                                                                                                                                    Query Match 68.3°
Best Local Similarity 95.0°
Matches 133; Conservative
                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
US-09-891-216-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 86; Conserv
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US-09-891-216-13
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                                                                                 LENGTH: 142
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Gaps

30;

Indels

Length 134;

Gaps

30;

Length 134; Indels

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APPLICATION NUMBER: US/10/115,515
FILING DATE: 03-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                   APPLICATION NUMBER: US/09/599,658
FILING DATE: 21-Unn-2000
APPLICATION NUMBER: 09/055,584
FILING DATE: 4-UNNE-1998
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Loughney, Kate
McAllister-Lucas, Linda M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-115-515-10
                                                                                                                                                                                                                              REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32706
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ferguson, Kenneth M. Francis, Sharron H.
                                                                                                                                                                                                                                                                                             TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 23, Application US/10115515
Publication No. US20030054992A1
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
Corbin, Jackie D.
                                                                                                                                                                                                                                                                                                            TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 875 amino acids
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.5%;
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                                                                                    PRIOR APPLICATION DATA:
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Best Local Similarity 46.1%
Matches 59; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Illinois
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Thomas, Melissa K.
INVENTION: Cyclic GMP-Specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphodiesterase Materials and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10;
                                                                                                                                     APPLICANT: Ramakrishnan, Shyam
TITLE OF INVENTION: Regulation of Human
TITLE OF INVENTION: Phosphodiesterase-Like Enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31.6%; Score 308.5; DB 1
43.7%; Pred. No. 9.1e-23;
iive 34; Mismatches 43
                                                                                                                                                                                              TILE REFERENCE: 02973.00511
CURRENT APPLICATION NUMBER: US/09/891,216
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/213,998
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/293,221
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: PCT/FP01/07289
PRIOR FILING DATE: 2001-06-25
PRIOR FILING DATE: 2001-06-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 20
SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 CSVLLLEDIESPVVKFTKSFEL 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corbin, Jackie D.
Ferguson, Kenneth M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-115-515-10; Sequence 10, Application US/10115515; Publication No. US20030054992A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Francis, Sharron H.
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                                                                               Sequence 3, Application US/09891216 Patent No. US20020103120A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Beavo, Joseph A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kadlecek, Ann
Loughney, Kate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
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Best Local Similarity
Matches 62; Conserva
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                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Rat
US-09-891-216-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF
                                                          US-09-891-216-3
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54 KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAIN-KIPEGAPFTEDDEKVMQMY 112
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237 EDPRFNAEVDQITGYKTQSILCMPIKNHREEVVGVAQAINKKSGNGGTFTEKDEKDFAAY
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Thomas, Melissa K.
TITLE OF INVENTION: Cyclic GMP-Specific FITLE OF Phosphodiesterase Materials and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 307.5; DB 9;
; Pred. No. 1.2e-22;
31; Mismatches 37;
ATTORNEY/AGENT INFORMATION:
NAME: No. US20030054992Aland, Greta E.
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Sequence 3. Application US/10094168B

| Publication No. US20030092156A1
| Publication No. US20030092156A1
| GENERAL INFORMATION:
| APPLICANT: Phillips, Stephen C.; Harrow, Ian
| APPLICANT: Bandman, Olga
| TITLE OF INVENTION: ANTIBODIES SPECIFICALLY BINDING CYCLIC NUCLEOTIDE PDES
| FILE REFERENCE: PF 0623-2 CIP
| CURRENT APPLICATION NUMBER: US/10/094,168B
| CURRENT FILING DATE: 2002-11-13
| PRIOR PAPLICATION NUMBER: US 09/595,514
| PRIOR PLING DATE: 1090-06-14
| PRIOR PAPLICATION NUMBER: US 09/226,741
| PRIOR PAPLICATION NUMBER: US 09/226,741
| PRIOR PELING DATE: 1999-01-07
| SOFTWARR: PROGRAM
| SOFTWARE: PROGRAM
| SOFTWARE: PROGRAM
| SOFTWARE: PROGRAM
| SOFTWARE: PROGRAM
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                                                            247 EDPRFNAEVDQITGYKTQSILCMPIKNHREEVVGVAQAINKKSGNGGTFTEKDEKDFAAY 306
                                                                                                                 113 LPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCER 172
                                                                                                                                            APPLICANT: Phillips, Stephen C.; Harrow, Ian APPLICANT: Phillips, Stephen C.; Harrow, Ian APPLICANT: Lanfear, Jerry; Fawcett, Lindsay
APPLICANT: Bandman, Olga
TITLE OF INVENTION: ANTBODIES SPECIFICALLY BINDING CYCLIC NUCLEOTIDE PDES FILE REFERENCE: PF-0629-2 CIP
CURRENT APPLICATION NUMBER: US/10/094,168B
PRIOR APPLICATION NUMBER: US 09/595,514
PRIOR FILING DATE: 2000-6-14
PRIOR FILING DATE: 1099-01-07
PRIOR FILING DATE: 1999-01-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 19.1%; Score 186; DB 9; Length 367; Best Local Similarity 29.7%; Pred. No. 8.4e-11; Matches 38; Conservative 35; Mismatches 37; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030092156A1 HSPDE10A2
US-10-094-168B-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                    173 CSVLLLED 180
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367 CTIFIVDE 374
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TYPE: PRT
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Sequence 5, Application US/10094168B
Publication No. US20030092156A1
Sequence 5, Application Sequence 5, Publication No. US20030092156A1
Sequence 5, Application No. US20030092156A1
APPLICANT: Innfear; Jerry: Fawcett, Lindsay
APPLICANT: Bandman, Olga
TITLE OF INVENTION: ANTIBODIES SPECIFICALLY BINDING CYCLIC NUCLEOTIDE PDES
FILE REFERENCE: PF-0623-2 CIP
CURRENT FILING DATE: 2002-11-13
PRIOR PELICATION NUMBER: US 09/595,514
PRIOR APPLICATION NUMBER: US 09/255,741
PRIOR APPLICATION NUMBER: US 09/226,741
SPRIOR FILING DATE: 1999-01-07
NUMBER 0F SEQ ID NOS: 7
SEQ ID NO 5
LENGTH 875
LENGTH 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 LPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCER 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 875;
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; OTHER INFORMATION: GenBank ID No. US20030092156A1 g3355606
US-10-094-168B-5
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                                                                                                      APPLICATION NUMBER: US/09/599,658
FILING DATE: 21-Jun-2000
APPLICATION NUMBER: 09/055,584
FILING DATE: 4-UUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: NO. US20030054992Aland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32706
APPLICATION NUMBER: US/10/115,515
FILING DATE: 03-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-115-515-23
                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 875 amino acids
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                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 CSVLLLED 180
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PIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYLPFCGIAISNAQLFAASRKEYERS 136
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Fatent No. US20020081633A1
GENERAL INFORMATION:
APPLICANT: KAPATION:
APPLICANT: Hunter, John Joseph
APPLICANT: Hunter, John Joseph
TITLE OF INVENTION: Methods for Using 22045, A Human Cyclic
TITLE OF INVENTION: Methods for Using 22045, A Human Cyclic
TITLE OF INVENTION: Methods for Using 22045, A Human Cyclic
TITLE REFERENCE: 5800-71
CURRENT APPLICATION NUMBER: US/09/420,190
CURRENT FILING DATE: 1999-10-18
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 779
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                                                                                                                                                                                                                                             Length 490;
                                                                                 TYPE: PRT ORGANISM: Homo sapiens ORGANISM: Homo sapiens FEATURE:
NAME/KEY: misc_feature
CTHER INFORMATION: Incyte ID No. US20030092156A1 HSPDE10A1
US-10-094-168B-1
                                                                                                                                                                                                                                        Query Match 19.1%; Score 186; DB 9; Length 49C Best Local Similarity 29.7%; Pred. No. 1.2e-10; Matches 38; Conservative 35; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                              34 SLAEKQEK -- HQDFLIQRQTKT--
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Matches 33; Conservative
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PERL Program
SEQ ID NO 1
LENGTH: 490
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ORGANISM: Homo sapiens
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Sequence:

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Database

Searched:

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Human phosphodiest Rat phosphodiester Human phosphodiest Human cyclic nucle Human phosphodiest Human phosphodiest A human phosphodie

Human phosphodiest

Human phosphodiest

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Result

Human phosphodiest Formula VII repres

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Type 11 phosphodiesterases and encoded genes with activity of hydrolyzing cyclic nucleotides, useful for studying intracellular
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AAY14991
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01-JUN-2000; 2000JP-0163875.
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                              WPI; 2001-418074/44..
N-PSDB; AAH46709:
WO200146436-A1.
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Drosophila melanog
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1559.921 Million cell updates/sec
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1 MLKQARRPLFRNVLSATQWK......VLLLEDIESPVVKFTKSFEL 194
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             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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                                                                                                                                                                                                                                                     9
                                                     novel
                                             The present invention provides the protein and coding sequences of nove human and rat type 11 phosphodiesterases (PDE11). These are useful for studying intracellular signal transduction mechanisms, in screening highly selective inhibitors as drugs for treating diseases associated with the enzymes and for the identification or selection of selective inhibitory action against multiple type phosphodiesterases. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cyclic nucleotide phosphodiesterase; PDEXV; sexual dysfunction;
cardiovascular disease; gastrointestinal disorder; corpus cavernosum;
kidney; liver; skeletal muscle; testis prostate; spleen.
                                                                                                                                                                                                 1 MLKQARRPLFRNVLSATQWKKVKITRLVQISGASLAEKQEKHQDFLIQRQTKTKDRRFND
                                                                                                                                                                                                             Human cyclic nucleotide phosphodiesterase and its nucleotide sequence useful for treating cardiovascular disorders, sexual dysfunction and screening for drugs to treat associated disorders
signal transduction mechanism and in screening highly-selective inhibitors as drugs with superior efficacy \cdot
                                                                                                                                                        Length 684;
                                                                                                                                                        Score 975; DB 22;
Pred. No. 5.5e-96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleotide phosphodiesterase PDEXV
                                                                                                                                                                              Mismatches
                             Page 49-51; 77pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                  ΑA
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                                                                                                                                                                                                                                                                                                                                                                                                 684
                                                                                                                                                                             0;
                                                                                                                                                        100.0%;
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                                                                                                                                                                                                                                                                                                                                     IESPVVKFTKSFEL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                  Local Similarity 100.
nes 194; Conservative
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                                                                                                                                      684 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAF62311
                                                                                                                                                                                                                                                                                                                                                                                                                                                             cyclic
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                                                                                                                                      Sequence
                                                                                                                                                                                                                                           61
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                                                                                                                                                        Query Match
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                              Claim
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Matches
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AAB35472
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61 EIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVWQMYLPFCGIAI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180
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The present invention describes the protein and coding sequences of the human cyclic nucleotide phosphodiesterase PDEXV. This enzyme is capable of catalysing the degradation of cyclic nucleotides. The sequences are useful in the treatment of cardiovascular, gastrointestinal, spleen, corpus cavernosum, kidney, liver, skeletal muscle, testis and prostate related disorders, and in the enhancement of the male erectile response and the treatment of female sexual dysfunction. The present sequence is the PDEXV protein.
                                                                                                                                                                                                                                                                                                                                                                                                                               1 MLKQARRPLFRNVLSATQWKKVKITRLVQISGASLAEKQEKHQDFLIQRQTKTKDRRFND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYLPFCGIAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Type 11 phosphodiestérases and encoded genes with activity of hydrolyzing cyclic nucleotides, useful for studying intracellular signal transduction mechanism and in screening highly-selective inhibitors as drugs with superior efficacy
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                                                                                                                                                                                                                                                                                              Length
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                                                                                                                                                                                                                                                                                         Score 975; DB 22;
Pred. No. 5.5e-96;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oda
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                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                            100.0%;
100.0%;
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01-JUN-2000; 2000JP-0163875.
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                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 194; Conserv
                                                                                                                                                                                                                                          684 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAH46710.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-SEP-2001
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sequence is a protein of the invention.
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                                                                                                                                                                                                                                                                                                                                               selective inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-418074/44.
                        934 AA;
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                                                                                                                                                                                                                                                                                                                                                                                       WO200146436-A1.
                                                                                                                                                                                                                                                                                                                                    type 11
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                                                                                                                                                                                                                                                                                                               Rat type 11
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                         Sèquence
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                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding sequences of novel human and rat type 11 phosphodiesterases (PDE11). These are useful for studying intracellular signal transduction mechanisms, in screening highly-selective inhibitors as drugs for treating diseases associated with the enzymes and for the identification or selection of selective inhibitory action against multiple type phosphodiesterases. The present
studying intracellular signal transduction mechanisms, in screening highly-selective inhibitors as drugs for treating diseases associated with the enzymes and for the identification or selection of selective inhibitory action against multiple type phosphodiesterases. The present sequence is a protein of the invention.
                                                                                                                                          1 MLKQARRPLFRNVLSATQWKKVKITRLVQISGASLAEKQEKHQDFLIQRQTKTKDRRFND
                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Type 11 phosphodiesterases and encoded genes with activity of ... Mydrolyzing cyclic nucleotides, useful for studying intracellular signal transduction mechanism and in screening highly-selective inhibitors as drugs with superior efficacy ...
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                                                                                                                                                                                                                                                                                                                                                                                                                      phosphodiesterase; PDE11; signal transduction;
                                                                                      Length 685;
                                                                                                          11; Indels
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                                                                                     Score 882; DB 22;
Pred. No. 5.7e-86;
                                                                                                                                                                                                                                                                                                                                                                                                 2
                                                                                                                                                                                                                                                                                                                                                                                                 Human type 11 phosphodiesterase SEQ ID NO:
                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 42-45; 77pp; Japanese:
                                                                                                                                                                                                                                                                                                                                 AAG62677 standard; Protein; 934 AA
                                                                                                        7;
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                                                                                    90.5%;
90.7%;
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                                                                                                                                                                                                                                                         IESPVVKFTKSFEL 194
                                                                                                                                                                                                                                                                   (first entry)
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                                                                                    Query Match 90.5
Best Local Similarity 90.7
Matches 176; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     Human; type 11 phosp
selective inhibition
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                                                                685 AA
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                                                                 Sequence
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                                                                                                KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYL 113
                                                                                                                                                                                             PFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC 173
                                                                                                                                                                                                                       The present invention provides the protein and coding sequences of novel mann and rat type 11 phosphodiesterases (PDEII). These are useful for studying intracellular signal transduction mechanisms, in screening highly-selective inhibitors as drugs for treating diseases associated with the enzymes and for the identification or selection of selective inhibitory action against multiple type phosphodiesterases. The present sequence is a protein of the invention.
                                                                                                                            Gaps
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Type 11 phosphodiesterases and encoded genes with activity of Mydrolyzing cyclic nucleotides, useful for studying intracellular signal transduction mechanism and in screening highly-selective inhibitors as drugs with superior efficacy
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Length 934;
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                                                  Indels
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Pred. No. 9.9e-67;
; Mismatches 0;
  22;
Score 709; DB 22
Pred. No. 3.7e-67
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phosphodiesterase SEQ ID NO: 39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oda K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 69-72; 77pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG62680 standard; Protein; 935 AA
                                                                                                                                                                                                                                                                                                                    SVLLLEDIESPVVKFTKSFEL
                                                                                                                                                                                                                                                                                              SVLLLEDIESPVVKFTKSFEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yuasa K, Kotera J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.3%;
97.9%;
72.78;
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01-JUN-2000; 2000JP-0163875.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                         Best Local Similarity 99.3
Matches 140; Conservative
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FCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCERCS 174

115

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The present invention relates to human phosphodiesterase (PDE)-like enzymes and their corresponding polynucleotides. The invention also relates to reagents which regulate PDE-like enzyme activity and reagents which bind to human PDE-like enzyme gene products which can be used to regulate degradation of cGMP. Sequences of the invention are useful for modulating the activity of a PDE-like enzyme in a disease such as urinary incontinence, benign prostate hyperplasia, erectile dysfunction, cancer, diabetes or cardiovascular disorder (e.g. ischemic diseases, myocardial infarction). The present sequence is human PDE-like enzyme.
                KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYL 113
                                                               PFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC 173
                                                                                Human; phosphodiesterase; PDE-like enzyme; benign prostate hyperplasia; urinary incontinence; erectile dysfunction; cardiovascular disorder; cancer; diabetes; ischaemic disease; myocardial infarction; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated polynucleotide encoding a human phosphodiesterase-like enzyme, useful for treating a disease such as urinary incontinence, benign prostate hyperplasia, erectile dysfunction, diabetes, cancer or cardiovascular disorder -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 665.5; DB 23; Length 142;
Pred. No. 1.3e-63;
3; Mismatches 3; Indels 1;
                                                                                                                                                                                                                                                                                                                                         Human phosphodiesterase (PDE)-like enzyme #2.
                                                                                                                                                 SVLLLEDIESPVVKFTKSFEL 444
                                                                                                                                                                                                                                        AAE17789 standard; Protein; 142 AA
                                                                                                                               SVLLLEDIESPVVKFTKSFEL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 25; Fig 5; 165pp; English.
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ilarity 95.0%;
Conservative
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2001US-293221P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JUN-2001; 2001WO-EP07289
                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                        vasodilator; cardiant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2002-090522/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 133; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FARB ) BAYER AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAD28571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ramakrishnan S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200200854-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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25-MAY-2001;
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54
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Human; phosphodiesterase; diabetes; ischemic heart disease; hypertension; nephritis; pancreatitis; ulcer; allergy; asthma; rheumatism; osteoporosis; pain; anxiety; schizophrenia; manic depressive psychosis; parkinson's disease; dementia; infectious disease; malignant tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes a human polypeptide which has phosphodiesterase activity. The phosphodiesterase polypeptide and polynucleotide are used for the treatment and prevention of diabetes, ischemic heart disease, hypertension, nephritis, pancreatitis, ulcers, allergies, asthma, rheumatism, osteoporosis, pain, anxiety, schizophrenia, manic depressive psychosis, Parkinson's disease, dementia, infectious diseases, and malignant tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 MQMYLPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nakamura Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                 Amino acid sequence of a human phosphodiesterase polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.0%; Score 429; DB 22; Length 576; 100.0%; Pred. No. 2.7e-37; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polypeptides with phosphodiesterase activity and DNA for t diabetes, ischemic heart disease, hypertension, nephritis, pancreatitis, ulcers, allergies, asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sugano S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kawabata A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KCERCSVLLLEDIESPVVKFTKSFEL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KCERCSVLLLEDIESPVVKFTKSFEL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 90-93; 105pp; Japanese.
                                                                                                                                              AA.
                                                         VLLLEDIESPVVKFTKSFEL 194
                                                                                                                                           AAG67533 standard; Protein; 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                07-MAR-2000; 2000JP-0061464.
10-JUL-2000; 2000JP-0208610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                     06-MAR-2001; 2001WO-JP01720.
                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haruoka M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-570769/64.
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Matches 86; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 576 AA;
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                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Miyaji H,
            61
                                                                                                                                                                        AAG67533;
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RESULT 8 AAE17788

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IGIAGMVAQTKQ-----MINIKEAYKDARFNCEIDLKTGYKTNAILCMPICNYEGDIIG 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VAQAINKIPEGAPFTEDDEKVMQMYLPFCGIAISNAQLFAASRKEYERSRALLEVVNDLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VQISGASLAEKQEKHQDFLIQRQTKTKDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ 1D NO 17847; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                      Drosophila melanogaster polypeptide SEQ ID NO 17847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ABB57737-ABB72072).
The sequence data for this patent did not form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid detection
                                                                                                                       Protein; 1232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-191637P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genes from Drosophila and interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 44.8
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1232 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ABL07788
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                                                                                                                                                                                                                                                                                                                                                                         WO200171042-A2.
                                                                                                                                                                                                                                                                                                pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2000;
                                                                                                                                                                                                 26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venter JC,
                      63
                                                                                                                                                             ABB63685;
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                                                                                                                     ABB63685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to human phosphodiesterase (PDE)-like enzymes and their corresponding polynucleotides. The invention also relates to reagents which regulate PDE-like enzyme activity and reagents which bind to human PDE-like enzyme gene products which can be used to regulate degradation of cGMP. Sequences of the invention are useful for modulating the activity of a PDE-like enzyme in a disease such as urinary incontinence, benign prostate hyperplasia, erectile dysfunction, cancer, diabetes or cardiovascular disorder (e.g. ischaemic diseases, myocardial infarction). The present sequence is human PDE-like enzyme.
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                                                                                                                                                                                                                                                                                                              43..46
/note= "Encoded by TAG TG AAA of the inverse complementary strand of the sequence shown as SEQ ID NO: 1 in figure 1 of the specification (AAD28570)'
                                                                                                                                         Human; phosphodiesterase; PDE-like enzyme; benign prostate hyperplasia;
urinary incontinence; erectile dysfunction; cardiovascular disorder;
cancer; diabetes; ischaemic disease; myocardial infarction; cytostatic;
vasodilator; cardiant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated polynucleotide encoding a human phosphodiesterase-like enzyme, useful for treating a disease such as urinary incontinence, benign prostate hyperplasia, erectile dysfunction, diabetes, cancer or cardiovascular disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Encoded by TGA of the inverse complementary
strand of the sequence shown as SEQ ID NO: 1 in figure
1 of the specification (AAD28570)"
                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Encoded by TAG of the inverse complementary strand of the sequence shown as SEQ ID NO: 1 in figure 1 of the specification (AAD28570)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 135;
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Pred. No. 1.6e-32;
                                                                                                                   Human phosphodiesterase (PDE)-like enzyme #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEKVMQMYLPFCGIAISNAQLFAASRKEYERSR-
                                                                                                                                                                                                                                                                                Location/Qualifiers
AAE17788 standard; Protein; 135 AA
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Local Similarity 68.3%;
Hes 82; Conservative
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2001US-293221P.
                                                                            (first entry)
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                                                                            16-MAY-2002
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Matches
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ABB08376 standard; Protein; 1284 AA

RESULT 11 ABB08376

ABB08376;

SFE 502

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DKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYLPFCGIAISN 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   capable of detecting 1000 or more genes from brosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -KTKDRRFNDEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention relates to an isolated nucleic acid detection reagent
                                                                                                                                              Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 42399; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1284;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               discloses genomic DNA sequences (ABL16176-ABL30511), exsequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                     Drosophila melanogaster polypeptide SEQ ID NO 42399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 349; DB 22;
; Pred. No. 3.3e-28;
41; Mismatches 57;
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                                                                                                                                                                                                                                                                                                                                                                                          Myers EW;
                           ABB71869 standard; Protein; 1284 AA
                                                                                                                                                                                                                                                                                                                                                                                          Li PWD,
                                                                                                                                                                                                                                                                                  23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                              23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            genes from Drosophila and interactions
                                                                                        (first entry)
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Best Local Similarity 38.2
Matches 73; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       442 KG--SFSRVFD 450
                                                                                                                                                                                           Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                        Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-656860/75.
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                                                                                                                                                               pharmaceutical
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                                                         ABB71869;
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RESULT 10
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polypeptide. Treated an argument of the invention may be described as cytostatic and antianaemic. Polypeptides and polynucleotides of the invention can be used to identify agents that modulate the activity of a transketolase-like enzyme. They are also useful for treating transketolase-like enzyme in they are also useful for treating transketolase-like enzyme disorder such as cancer, anaemia, end-stage renal disease and sensory neuropathy associated with uraemia. Therapeutic agents of the invention are useful for modulating the activity of transketolase-like enzyme in the above mentioned diseases. Polypeptides and polynucleotides os the invention are useful for identifying test compounds which act as agonists or antagonists, for raising specific antibodies, and as a bait protein in a two-hybrid or three-hybrid assay. They are also useful in diagnostic assays for detecting diseases and abnormalities or susceptibility to disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 AQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCERCSVLLLEDIE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated human transketolase-like enzyme polypeptide, useful for treating cancer, anaemia, end-stage renal disease and sensory neuropathy associated with uraemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transkelotase like enzyme encoding sequence. Fusion proteins including the polypeptide of the invention may be useful in the generation of antibodies and in various assay systems. The current sequence represent the D. melanogaster CG10231 gene product that was used to aid the
                                                                                                                                          Transkelotase-like; enzyme; fruitfly; cytostatic; antianaemic; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYLPFCGIAISN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to an isolated transketolase-like enzyme
                                                                                                                                                                          anaemia; end-stage renal disease; sensory neuropathy; uraemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 KKVKITRLVQISGASLAEKQEKHQDFLIQRQT-
                                                                 D. melanogaster CG10231 gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 5; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2001; 2001WO-EP06125.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ramakrishnan S;
                                                                                                                                                                                                                                                                                                                    WO200192310-A2
07-MAY-2002
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence is a fragment of the human cGMP-binding phosphodiesterase (cGB-PDE), consisting of amino acid residues 1-494. The novel polypeptide can be used for the detection of cGB-PDE and the isolation of its expression control sequences. It can also be used to identify genetic alterations in the cGB-PDE locus associated with diseases. Antibodies specific for cGB-PDE fragments can also be used in detecting and quantifying the amount of cGB-PDE present in samples. (Note: this sequence is not given in the specification but is generated from the defined wild type sequence).
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EDPRENAEVDQITGYKTQSILCMPIKNHREEVVGVAQAINKKSGNGGTFTEKDEKDFAAY
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                                                                                                                                                                                                                                                                                                                                                       Human cGMP-binding phosphodiesterase; cGB-PDE; control sequence; antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.5%; Score 307.5; DB 19; Length 494; 46.1%; Pred. No. 2.6e-24; Indels 1; Mismatches 37; Indels 1;
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Lucas LM, Sonnenburg WK,
                                                                                                                                                                                                                                                                                                                                 phosphodiesterase fragment 2.
                                                                                                                                                                                                      AAW42013 standard; protein; 494 AA.
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Best Local Similarity 46.1
Matches 59; Conservative
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(UYVA-) UNIV VANDERBILT.
(UNIW ) UNIV WASHINGTON.
                                                            183 SPVVKFTKSFE 193
                                                                                                 442 KG--SFSRVFD 450
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                                                                                                                                                                                                                                                                                                                             cGMP-binding
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27-MAY-1993;
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antibody.
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Thomas MK;
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-Lucas LM, Sonnenburg WK,
                                                                                                                                                                       cGMP-binding phosphodiesterase fragment 3.
                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
AAW42014 standard; protein; 549 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beavo JA, Corbin JD, Ferguson b
Loughney K, McAllister-Lucas LM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94US-0250847.
93US-0068051.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94US-0250847
                                                                                                              (first entry)
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Best Local Similarity 46.1%
Matches 59, Conservative
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est Local Similarity
                                                                                                                                                                                                                                                                                                                                                 832 AA;
                                                                                                                                                                                             N-PSDB; AAZ95234.
 atherosclerosis,
                                                 WO200005383-A1
                              Homo sapiens
                                                                                                                        16-APR-1999;
                                                                                                             21-JUL-1998;
                                                                     03-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                              202
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                                                                                                                                                               Tarui N,
                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                This sequence represents a human phosphodiesterase V amino acid sequence. The phosphodiesterase V protein, its fragments and salts are useful in the identification of phosphodiesterase V inhibitors for use in the treatment of hypertension, pulmonary hypertension, atherosclerosis, cerebral infarction, allergic rhinitis, kidney failure, diabetic complications, and glaucoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAIN-KIPEGAPFTEDDEKVMQMY 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCER 172
                                                                              Phosphodiesterase V; human; hypertension; pulmonary hypertension; atherosclerosis, cerebral infarction; allergic rhinitis; kidney failure; diabetic complication; glaucoma.
                                                                                                                                                                                                                                                                                                      New phosphodiesterase V useful for screening potential phosphodiesterase inhibitors for treatment of hypertensive and allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phosphodiesterase V; human; hypertension; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 832;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21;
                                                           Human phosphodiesterase V amino acid sequence #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human phosphodiesterase V amino acid sequence #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.5%; Score 307.5; DB 2 46.1%; Pred. No. 5.3e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31; Mismatches
                                                                                                                                                                                                                                                                                                                                               Disclosure, Fig 5-6; 96pp; Japanese.
AAY78939 standard; Protein; 832 AA
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                                                                                                                                                                                                                                                     Doi T, Nakahama K;
                                                                                                                                                                                 99WO-JP03865.
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                                                                                                                                                                                                              99JP-0108974
                                                                                                                                                                                                                                 (TAKE ) TAKEDA CHEM IND LTD.
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Best Local Similarity 46.19
Matches 59; Conservative
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                                                                                                                                                                                                                                                                        WPI; 2000-182705/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                      832 AA;
                                                                                                                                                                                                                                                                                   N-PSDB; AAZ95233
                                                                                                                                          WO200005383-A1
                                                                                                                       Homo sapiens.
                                                                                                                                                                                19-JUL-1999;
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                                       05-JUN-2000
                                                                                                                                                                                                     21-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents a human phosphodiesterase V amino acid sequeste phosphodiesterase V protein, its fragments and salts are useful the identification of phosphodiesterase V inhibitors for use in the treatment of hypertension, pulmonary hypertension, atherosclerosis, cerebral infarction, allegic rhinitis, kidney failure, diabetic complications, and glaucoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31; Mismatches
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Job time : 16.5718 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Page 88-90; 96pp; Japanese.
                                diabetic complication; glaucoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Doi T, Nakahama K;
                                                                                                                                                                                                                                                                                                                                                98JP-0204964.
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June 13, 2003, 15:44:04; Search time 12.8155 Seconds (without alignments) 3119.127 Million cell updates/sec
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975
1 MLKQARRPLFRNVLSATQWK......VLLLEDIESPVVKFTKSFEL 194
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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sp_phage:*
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1: sp_archea:*
2: sp_bacteria:*
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Maximum DB seq length: 2000000000
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sp_mhc:*
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		•				
Result No.	Score	Query Match	å Query Match Length DB	DB	ID	Description
1	975	100.0		4	09GZY7	O9qzv7 homo sapien
7	882	90.5		11	O8VID7	O8vid7 rattus norv
e	813	83.4		4	096876	096s76 homo sapien
4	709	72.7		4	O9HCR9	Oghcr9 homo sapien
ۍ	705	72.3		11	Q8VID6	O8vid6 rattus norv
9	433	44.4		11	Q8VID8	O8vid8 rattus norv
7	429	44.0		4	Q9HB46	O9hb46 homo sapien
æ	354.5	36.4		വ	Q95TW8	095tw8 drosophila
6	354.5	36.4		Ŋ	Q9VFI9	Ogvfi9 drosophila
10	349	35.8		2	67579	09vi79 drosophila
11	203	20.8		2	Q9GQU6	Oggane trypanosoma
12	201	20.6		11	Q8R0D4	O8rOd4 mus musculu
13	201	20.6		11	091201	091zgl mus musculu
14	199	20.4		Ŋ	Q8WQX9	Q8wqx9 trypanosoma
15	189.5	19.4	819	'n	920960	096076 ephydatia f
16	186	19.1		4	09NY45	Ognv45 homo sapien

5 rana canis		Q8uuy7 rana pipien		P94182 anabaena sp	Q8yvs0 anabaena sp	P94181 anabaena sp	Q9ntv4 homo sapien	Q9hcp9 homo sapien	Q9wvil mus musculu	Q9qyj5 rattus norv	Q9ulw9 homo sapien	Q9qyj6 rattus norv	Q9gtn9 trypanosoma	Q8yv44 anabaena sp	Q9f5y4 anabaena va	096195 plasmodium	Q8yyg4 anabaena sp	Q9ud49 homo sapien	Q9xbm4 myxococcus	. Q8yn83 anabaena sp	O53473 mycobacteri	Q9qyt5 rattus norv	Q8yzy1 anabaena sp			Q91708 anabaena sp
Q8UUY5 O97746	OSUUY6 QBUUY6	Q800Y7	062037	P94182	Q8YVS0	P94181	Q9NTV4	бансь	Q9WVI1	Q9QYJ5	O9ULW9	090YJ6	O9GTN9	Q8YV44	Q9F5Y4	096195	Q8YYG4	Q9UD49	Q9XBM4	Q8YN83	053473	Q9QYT5	Q8YZY1	P95194	Q971R4	Q9L708
13	13	13	11	. 5	16	16	4	4	11	11	4	11	S	16	7	S	16	4	7	16	16	11	16	16	17	16
861	857	866	800	860	860	859	657	714	779	788	789	794	485	944	445	1245	1850	101	773	1900	573	235	1808	578	540	1777
19.0	18.6	18.6	18.5	18.3	18.3	17.9	16.9	16.9	16.9	16.9	16.9	16.9	16.9	13.2	12.2	12.2	12.2	12.0	12.0	11.9	11.4	10.7	9.7	9.7	9.6	9.6
183	181.5	181.5	180	178.5	178.5	174.5	165	165	165	165	165	165	164.5	129	118.5	118.5	118.5	117	117	116	111.5	104	95	94.5	94	94
17	20	21	22	23	24	25	26	27	28	29	30	31	32	. 33	34	35	36	37	38	39	40	. 41	42	43	44	45

## ALIGNMENTS

0.96	Q9GZY7 PRELIMIN Q9GZY7, 01-MAR-2001 (TrEMBLr 01-MAR-2001 (TrEMBLr 01-UNA-2002 (TrEMBLr CAMP/CGMP CYCLIC nuC 11A2). PDELIA3 OR HSPDELIA. HOMO SAPIENS (Human) Eukaryota; Metazoa; Mammalia; Eutheria; NCBL_TAXID-9606; [1] SEQUENCE FROM N.A. SEGUENCE FROM N.A.	7977 PRELIMINARY; PRT; 962X7 PGGXY; 0962X7; 01-MAR-2001 (TrEMBLrel. 16, Last s 01-MAR-2001 (TrEMBLrel. 11, Last s 01-JUN-2002 (TrEMBLrel. 21, Last s cAMP/cGMP cyclic nucleotide phosph 11A2). PDE11A3 OR HSPDE11A. Homo sapiens (Human). BLKaryota; Metazoa; Chordata; Cran Mammalia; Eutheria; Primates; Cata NCBLTAXID=9606; 11]	PRT; 684 AA.  Created) Last sequence update) Last annotation updat phosphodiesterase 11A  a; Craniata; Vertebrat s; Catarrhini; Hominid	684 / ence tatio ester ester a; Vé ini;	PRT; 684 AA.  Created) Last sequence update) Last annotation update) phosphodiesterase 11A3 (Phospi ; Craniata; Vertebrata; Eutele; ; Catarrhini; Hominidae; Homo	PRT; 684 AA.  Created) Last sequence update) Last annotation update) phosphodiesterase 11A3 (Phosphodiesterase ; Craniata; Vertebrata; Euteleostomi; ; Catarrhini; Hominidae; Homo.
RA R	Hetman J.M., Robas N.M. Soderling S.H., Beavo J. Cloning and characteri, phosphodiesterase 11A." Proc. Natl. Acad. Sci. [2] SEQUENCE FROM N.A. TISSUE=TESTIS; MEDLINE=20469516; Pubme Fusas K., Kotera J., Fu "Isolation and Characte Variants Showing Unique J. Biol. Chem. 275:3146 EMBL; AU278682; CAC1556 EMBL; AB038041; BAB1637 InterPro; IPR0030318; GA InterPro; IPR0030318; GAF; 2. Pfam; PF00533; PDESSES	Hetman J.M., Robas N.M., Baxendale R., Fidock Soderling S.H., Beavo J.A.;  "Cloning and characterisation of two splice v phosphodiesterase 11A.";  Proc. Natl. Acad. Sci. U.S.A. 97:12891-12895( [12]  SEQUENCE FROM N.A. TISSUE-TESTIS  MEDLINE=20469516; PubMed=10906126;  Widasa K., Kotera J., Fujishige K., Michibata "Isolation and Characterization of Two Novel Variants Showing Unique Structure and Tissue-Ariants Showing Unique Structure and Tissue-MEDI. AJ278682; CAC15567.1;  EMBL, AJ278682; CAC15567.1;  InterPro: IPR003018; GAF.  InterPro: IPR003018; GAF.  InterPro: IPR003018; GAF.  InterPro: IPR003018; PDEase.  Pfani, PP01539() GAF; 2.  Pfani, PP01539; PDEase: 1.  PRINTS; PR0033; PDEASE: 1.	Baxendale R.  Lin of two S.A. 97:1289 S.A. 97:1289 Shige K., Mi zation of Tw tructure and 31479(2000).  Li - Pplase_HDC. ise.	splic 1-128 chiba o Nov Tiss	dale R., Fidock M., Phillips of two splice variants of hur 97:12891-12895(2000). 126; K., Michibata H., Sasaki T., n of Two Novel Phosphodiester ure and Tissue-specific Expre (2000)HDC.	Herman J.M., Robas N.M., Baxendale R., Fidock M., Phillips S.C., Soderling S.H., Beavo J.A.; "Cloning and characterisation of two splice variants of human phosphodiesterase 11A."; Proc. Natl. Acad. Sci. U.S.A. 97:12891-12895(2000).  EXCUENCE FROM N.A. TISSUE-FERSITE SEQUENCE FROM N.A.  TISSUE-FERSITE TISSUE-FERSUE TISSUE-FERSITE TISSUE-FERSITE TISSUE-FERSUE TISSUE-FERSUE TISSUE-FERSUE TISSUE-FERSUE TISSUE-FERSUE TISSUE-FERSUE TISSUE-FERS

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InterPro; IPR002073; PDEase.
Pfam; PF01590; GAF; 2.
                                                                                              01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel, 19,
                                                                                                                                                                                                                                                                                                                                                                                                   AB048415; BAB62713.1;
AB048416; BAB62713.1;
AB048417; BAB62713.1;
             AB048418; BAB62713.1;
  IESPVVKFTKSFEL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                             AB048419; BAB62713.1;
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BAB62713.1
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Matches 194; Conservative
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                                                                           PRELIMINARY;
                                                                                                          01-DEC-2001 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.
                                                                                                                               Phosphodiesterase 11A3.
                                                                                                                                         Homo sapiens (Human)
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    AB048409; E
AB048410; E
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                     181
  181
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                                                                                                                                       1 MLKQARRPLFRNVLSATQWKKVKITRLVQISGASLAEKQEKHQDFLIQRQTKTKDRRFND
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
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                                                               ;
                                         Length 684;
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                                                               Indels
                    1E41C4F5199D6B1E CRC64;
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Last annotation update)
                                        Score 975; DB 4;
Pred. No. 3.8e-74;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                        685 AA
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        PROSITE; PS00126; PDEASE_I; 1. SEQUENCE 684 AA; 78133 MW;
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Best Local Similarity 100.
Matches 194; Conservative
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01-MAR-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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SMART; SM00471; HDC; 1.
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61 DFGEVETFLDRHPELFEDYLMRKGKQEMVEKWLQRHSQGQGALGPRPSLAGTSSLAHSTC 120
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Yuasa K., Kanoh Y., Okumura K., Omori K.;
Genomic organization of the human phosphodiesterase PDE11A gene:
Evolutionary relatedness with other PDEs containing GAF domains.";
Eur. J. Biochem. 268:168-178(2001).
                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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988 AA; 111170 MW; 7F678869353DF7EB CRC64;
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Pred. No. 2.9e-60;
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EMBL; AB048423; BAB62713.1; -.
EMBL; AB048402; BAB62713.1; JOINED.
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AB048404; BAB62713.1; JOINED.
AB048405; BAB62713.1; JOINED.
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X Yuasa K., Kanoh Y., Okumura K., Omori K.;

Y Yuasa K., Kanoh Y., Okumura K., Omori K.;

T "Genomic organization of the human phosphodiesterase PDE11A gene:
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                      PTAIDYKCHLKKHNERQFFLELVKDISNDLDLTSLSYKILIFVCLMVDADRCSLFLVEGA
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Yuasa K., Kotera J., Fujishige K., Michibata H., Sasaki T., Omori K.
"Isolation and Characterization of Two Novel Phosphodiesterase PDE11
Variants Showing Unique Structure and Tissue-specific Expression.";
J. Biol. Chem. 275:31469-31479(2000).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Phosphodiesterase 11A (Phosphodiesterase 11A4).
HSPDELIA
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InterPro; IPR002073; PDEase.
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                                                                                                                                                                                                                                                       364 PFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 PFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYL
                                                                                                                                                                                                                                 54 KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYL
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                                                                                                                                                                                        Gaps
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Yuasa K., Ohgaru T., Asahina M., Omori K.;
Young T., Omparison of rat and human PDE11A splicing variants.";
Eur. J. Blochem. 268:4440-4448(2001).
Eur. J. Blochem. 268:4440-4448(2001).
InterPro; IPR003018; Ag.
InterPro; IPR003018; Ag.
InterPro; IPR003073; PDEase.
Pfam; PF00333; PDEase: 1.
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SMART; SM00065; GAF; 2.
SMART; SM00471; HDC; 1.
PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
SEQUENCE 935 AA; 104570 WW; E80F1039770F8276 CRC64;
                                                                                                     994675824259447E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                           72.7%; Score 709; DB 4; 199.3%; Pred. No. 1.7e-51; ive 1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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Pfam; PF00233; PDEase; 1.
PRINTS; PR00387; PDIESTERASE1.
SMART; SM00065; GAF; 2.
SMART; SM00471; HDC; 1.
PROSITE; PS00126; PDEASE_I; 1.
SEQUENCE 934 AA; 104810 MW; 9
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                                                                                                                                                                   Best Local Similarity
Matches 140; Conserv
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01-JUN-2002
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nes 138;
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191
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                                                                                                               Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 VMQMYLPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTL 63
                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Yuasa K., Ohgaru T., Asahina M., Omori K.;
Identification of rat cyclic nucleotide phosphodiesterase 11A
(PDE11A): comparison of rat and human PDE11A splicing variants.";
Eur. J. Blochem. 268:4440-4448(2001).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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"Cloning and characterization of two splice variants of human phosphodiesterase 11A.";
Proc. Natl. Acad. Sci. U.S.A. 97:12891-12895(2000).
EMBL: AF281865; AAG32023.1;
InterPro: IPR003018; GAF.
InterPro: IPR003018; ME.Pplase_HDc.
InterPro: IPR003073; PDEase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44.4%; Score 433; DB 11; Length 5
100.0%; Pred. No. 1.9e-28;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00126; PDEASE_I; UNKNOWN_I.
SEQUENCE 581 AA; 66141 MW; 2CA7C2F5DDB37D00 CRC64;
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1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
cAMP/CGMP phosphodiesterase 11A2.
                                                                                                           Last sequence update)
Last annotation update)
                                           581 AA
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InterPro; IPR003018; GAF.
InterPro; IPR003077; ME_Pplase_HDc.
InterPro; IPR002073; PDEase.
Pfam; PF01590; GAF; 1.
Pfam; PF00233; PDEase: 1.
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SMART; SM00065; GAF; 1.
SMART; SM00471; HDC; 1.
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Matches 87; Conservative
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                                           PRELIMINARY;
                                                                                                           (TrEMBLrel.
                                                                                      01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                    Rattus norvegicus (Rat)
                                                                                                        01-MAR-2002 (TrEMBLrel
01-JUN-2002 (TrEMBLrel
Phosphodiesterase 11A2
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Q9HB46;
                                         Q8VID8
RESULT 6
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                      Q8VID8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 EEQTDLEKIVKKIMHRAQTLLKCERCSVLLLE------DIESP-----VVKFTK 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 VQISGASLAEKQEKHQDFLIQRQTKTKDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                  Gaps
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Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.,
Submitted (COT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AV058470; AAL13699.1.
FlyBase, FBgn0038237; C68279.
InterPro; IPR003018; GAF.
InterPro; IPR003018; Parase.
PinterPro; PR001330; Prenyl_site.
Pfam; PF01590; GAF; 2.
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                                                                                                                                 Length 576;
                                                                                                                                                                             Indels
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PROSITE; PS00294; PRENYLATION; UNKNOWN_I.
SEQUENCE 1018 AA; 114668 MW; 8C758A607855EDD9 CRC64;
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SMART; SM00065; GAF; 1.
SMART; SM04071; HDc; 1.
PROSTTE; PS00126; PDEASE_I; 1.
SEQUENCE 576 AA; 65766 MW; 3992C4C95A5B0B36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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44.8%; Pred No 1.6e-21;
M.cmarches 55;
                                                                                                                            44.0%; Score 429; DB 4; I
100.0%; Pred. No. 4.2e-28;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1018 AA
                                                                                                                                                                                                                                                                                                                                 KCERCSVLLLEDIESPVVKFTKSFEL 194
                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100. Matches 86, Conservative
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01-DEC-2001 (
01-JUN-2002 (
GH27433P.
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., R.A. Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.E., Gocayne D.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Ramanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N., Gotoge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Radon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Radon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Radon R.C., Baxter E.G., Helf G., Nalson C.R., Mixloo G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Raderson R.Y., Beacos P.V., Berman B.P., Bhandari D., Bolshakov S., Burkova D., Botchan M.R., Bauck J., Brokstein P., Brottier P., Botchav S., Dahlke C., Davenport L.B., Davies P., Abril J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Abril J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Burbin R.J., Evangelista C.C., Ferraz C., Ferraz C., Ferraz C., Gabriellan A.E., Garral L.B., Davies P., Bolds R.A., Gong F., Gornell J.H., Ralush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Houston K.J., Houston K.J., Hernandez J.R., Houck J., Harris M., Alush F., Karpen G.H., Ke Z., Gulbart W., Gabriellan R., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Moutt S.M., Marphy B., Murphy L., Muzray D.M., Nelson D.L., Moutt S.M., Mout K.M., May M., Murphy B., Murphy L., Muzray D.M., Nelson D.L., Shidh K., Shingson M., Stupski M.P., Santh T., Shingson M., Shusker D.M., Wang X., Wangage T., Shap K., Wangaman D.A., Wencer E., Wang K., Wanliams S.M., Woodage T., Shap K., Wangaman D.A., Wenter E., Wang K., Wallen S., Choeler F., Shen H., Wang X., Whyers E.W., Robin G.M., Venter E., Wang K., Shing K., Shing K., Shing K., Wangaman D.A., Wang X., Zhan M., Zhang S., Change S., Change S., Chang S., Change S., Chang S
                                                                                                                                                                                                                                    Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00126; PDEASE_I; 1.
PROSITE; PS00294; PRENYLATION; UNKNOWN_I.
SEQUENCE 1232 AA; 137426 MW; ECF6B9G3A71BAF74 CRC64;
                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                            PRT; 1232 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003018; GAF.
InterPro; IPR003607; ME_Pplase_HDC.
InterPro; IPR002073; PDEase.
Pfam; PF01590; GAF; 2.
Pfam; PF00533; PDEase; 1.
                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20196006; Pubmed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00387; PDIESTERASE1.
SMART; SM00065; GAF; 2.
SMART; SM00471; HDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE003705; AAF55066.2; FlyBase; FBgn0038237; CG8279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 287:2185-2195(2000).
                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    Ephydroidea; Dro
                                                                                                                                                                                                                                                                                                                                             STRAIN-BERKELEY;
                                                                                                                                                CG8279 protein.
                                                                                                                                                                        CG8279
                                            O9VFI9
RESULT 9
Q9VFI9
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Length 1232;

DB 5;

Score 354.5; DB 5 Pred. No. 2.1e-21;

36.48;

Query Match Best Local Similarity

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Amentides P.C., Scherer S.E., 11P P.W., Hoskins R.A., Galle R.F.,
Amentides P.C., Scherer S.E., 11P P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.C., Scherer S.E., 11P P.W., Hoskins R.A., Galle R.F.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rayers Y. H.C., Blazel R.G., Champhe M., Pfelfefre B.D.,
RA Abril J.E., Abbayani A. An H.-J., Andrews-Pfannkoch C., Baldwin D.D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Charer P.A., Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chare Pablos B., Daller H., Cadieu E., Center A., Chun P.,
Burtis K.C., Beangelista C.C., Ferraz C., Ferriac E., Pleischman W.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriac S., Fleischman W.,
RA Color C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,
Andrey D., Howland T.J., Wei M.-H., Ibeywam C.,
Alali M., Ralush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Basko P., Lei Y., Lavitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattel B., Moritosh T.C., McLeod M.P., Morits J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Ra Alazzolo M., Nelson K.A., Nixon K., Noris S., Shen H.,
Rainert K., Remington K., Saunders R.D., Scheller F., Shen H.,
Rainert K., Remington K., Saunders R.D., Scheller F., Shen H.,
Rayier E., Spradling A.C., Stapeleton M., Strong R., Sun E.,
Rayier E., Stapelling A.C., Stapeleton M., Strong R., Sun E.,
Rayier E., Stapelling G., Zangeling G., Zhan W., Zhu S., Zhu S., Zhu S., Shith D.,
Rayier E., Stapelling G., Zangeling G., Zhun E., Sheng K., Zh
                                                               88 VAQAINKIPEGAPFTEDDEKVMQMYLPFCGIAISNAQLFAASRKEYERSRALLEVVNDLF 147
                                                                                                                                                                                                                   148 EEQTDLEKIVKKIMHRAQTLLKCERCSVLLLE*****DIESP*****VVKFTK 190
                                                                                                                                                                                                                                          28 VQISGASLAEKQEKHQDFLIQRQTKTKDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIG 87
                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
23;
  55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CG10231 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1284 AA.
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20196006; PubMed=10731132;
  23;
82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                       191 SFE 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=7227;
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  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                       09VJ79
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NCBI_TaxID=10090;
           105
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                                                                                                         RESULT 12
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oy
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                                                                                                                                          δλ
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DTT
DDT
DDT
DDT
DDT
CO
OOC
OOC
OOC
NXT
RRA
RRA
DR
DR
DR
                                                                                                                                                                                                                                                  DKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMYLPFCGIAISN 122
                                                                                                                                                                                                                                                            AQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCERCSVLLLEDIE 182
                                                                                                                                                                                                                                                                                                        55 DRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINK------IPEGAPFTED 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rascon A., Soderling S.H., Beavo J.A.;
"Cloning and characterization of a cyclic nucleotide phosphodiesterase from Trypanosoma brucel.";
submitted cosoma brucel.";
Submitted AF192755, AAG43461.1;
InterPro; IPR003018; GAF.
InterPro; IPR003067; ME_Pplase_HDc.
InterPro; IPR002073; PbEase.
Pfam; PF01590; GAF; 2.
                                                                                                                                                                                                                       20 KKVKITRLVQISGASLAEKQEKHQDFLIQRQT------KTKDRRFNDE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBL_TaxID=5691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                Length 1284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43; Indels
                                                                                                                            PROSITE; PS00126; PDEASE_I; 1.
SEQUENCE 1284 AA; 141726 MW; F6873C90A9953430 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00126; PDEASE_I; 1.
SEQUENCE 930 AA; 103269 MW; 4E297F6347F59A29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Cyclic nucleotide phosphodiesterase.
"The genome sequence of Drosophila melanogaster.";
                                                                                                                                                             35.8%; Score 349; DB 5;
38.2%; Pred. No. 6.4e-21;
iive 41; Mismatches 57,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.8%; Score 203; DB 5; 35.3%; Pred. No. 9.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                930 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31; Mismatches
                                        Interpro; IPR003018; GAF.
Interpro; IPR003007; ME_Pplase_HDC.
Interpro; IPR002073; PDEase.
Pfam; PF01590; GAF; 2.
Pfam; PF00233; PDEase; 1.
PRINTS; PR00387; PDIESTERASE1.
SMART; SM0065; GAF; 2.
SMART; SM00471; HDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
         Science 287:2185-2195(2000).
EMBL; AE003659; AAF53675.1; -.
FlyBase; FBgn0032686; CG10231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0387; PDIESTERASE1.
SMART; SM00065; GAF; 2.
SMART; SM00471; HDC; 1.
                                                                                                                                                                       Local Similarity 38.2 ies 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48; Conservative
                                                                                                                                                                                                                                                                                                                                                           442 KG--SFSRVFD 450
                                                                                                                                                                                                                                                                                                                                      SPVVKFTKSFE 193
                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trypanosoma brucei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                  63
                                                                                                                                                                                                                                                                                             123
                                                                                                                                                                                                                                                                                                                382
                                                                                                                                                                                                                                                                                                                                     183
                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                               900560
                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
Q9GQU6
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g
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DEKVMQMYLPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFE-EQTDLEKIVKKIMHR 163
                              113 LPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAP-FTEDDEKVMQMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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"A sequence alteration in Pde6c gene causes cone photoreceptor function loss (cpfl1) in mice.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF411063; AAK96254.1;
"MGD; MGR1:105956; Pde6c.
InterPro; IPR003018; GAF.
InterPro; IPR003013; PDEase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=RETINA;
Chang B., Hawes N.L., Hurd R.E., Davisson M.T., Nusinowitz S.,
                                                                                                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to phosphodiesterase 6C, cGMP specific, cone, alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases. Submitted (APR-2005). AR427050.1; -. SEQUENCE 836 AA; 95906 MW; A8D60FAAFE6C9D9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.6%; Score 201; DB 11; 37.8%; Pred. No. 1.2e-08; iive 26; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 861 AA.
                                                                                                                                                                                                                                                                                         836 AA
                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                  164 AQTLLKCERCSVLLLE 179
                                                                                                                                     |: || :| |: |:: |:: 419 AKKLLNADRSTLFLVD 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cGMP phosphodiesterase 6c.
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                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          091ZQ1;
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 CSVLLLE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1: ||:
277 YSIGLLD 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=EYE;
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819 AA

PRELIMINARY;

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Search co
                                                                                                                                                                                                                                                                                                                                                                                               113 LPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLLKCER 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 KDRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAP-FTEDDEKVMQMY 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 DRRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINK------IPEGAPFTED 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105 DEKVMQMYLPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFE-EQTDLEKIVKKIMHR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trypanosoma brucei.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma
NCBI_TaxID=5691;
                                                                                                                                                                                                                                                                                                     4;
                                                                                                                                                                                                                                  Length 861;
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                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jonath R., Seebeck T.;
Zoraghi R., Seebeck T.;
Phosphodiesterase TbPDE2C from Trypanosoma brucei.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ-databases.
EMBL: AYO2044 AAK33016.1;
InterPro; IPR003018; GAF.
InterPro; IPR003507; ME_Pplase_HDC.
InterPro; IPR002073; PDEase.
Pfam; PF01590; GAF; 2.
Pfam; PF0153; PDEase.
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SEQUENCE 930 AA; 103694 MW; 1D5A12E39818C807 GRC64;
InterPro; IPR001230; Prenyl_site.
Pfam; PF01590; GAF; 2.
Pfam; PF00233; PDEasE; 2.
PF03TTE; PS00126; PRENYLATION; UNKNOWN_1.
PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
SEQUENCE 861 AA; 98785 MW; C582D78114652B5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L'MAR-2002 (TrEMBLrel. 20, Created)
L-MAR-2002 (TrEMBLrel. 20, Last sequence update)
L-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                           20.6%; Score 201; DB 11;
37.8%; Pred. No. 1.2e-08;
ative 26; Mismatches 49;
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SMART; SM00065; GAF; 2.
SMART; SM00471; HDC; 1.
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Best Local Similarity 34.6%
Matches 47; Conservative
                                                                                                                                                                                                                        Query Match . 20.68
Best Local Similarity 37.89
Matches 48; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 CSVLLLE 179
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277 YSIGLLD 283
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completed: June 13, 2003, 15:48:49 ne: 13.8155 secs

RESULT 15 096076

335 AERCSLFLLDKSRSNLV

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54 KDRRFNDEIDKLTGYKTKSLLCMPI--RSSDG--EIIGVAQAINKIPEGAPFTEDDEKVM 109
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                                                                                                                                                                       X MEDLINE-99015760; PubMed-9801141;
A KOYANGAI M., Suga H., Hoshlyama D., Ono K., Iwabe N., Kuma K.,
Miyata T.;
Andlent gene duplication and domain shuffling in the animal cyclic
T "Ancleotide phosphodiesterase family.";
FEBS Lett. 436:1393-328(1998).
R EMBL, AB017022; BAA34308.1;
R InterPro; IPR003018; GAF.
R InterPro; IPR003018; Pabase.HDc.
R InterPro; IPR002033; Pabase.
R Pfam; PF01590; GAF. 2.
R Pfam; PF01533; Pabase: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 819;
                                                                                                        Eukaryota: Metazoa; Porifera; Demospongiae; Ceractinomorpha;
Haplosclerida; Spongillidae; Ephydatia.
NCBL_TaxID=31330;
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SMART; SM00065; GAF; 2.
SMART; SM00471; HDC; 1.
PROSITE; PS00126; PDEASE I; 1.
SEQUENCE 819 AA; 92145 MW; F4CA1EE8B23A9E0E CRC64;
                           01-WAY-1999 (TrEMBLrel. 10, Created)
01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.4%; Score 189.5; DB 5; 32.8%; Pred. No. 1.1e-07; tive 29; Mismatches 58;
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01-MAY-1999
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:

June 20, 2003, 10:43:55 ; Search time 5414 Seconds.
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US-09-663-542-2 2078 1 ggtccgagatgctgaagcag.....actaataactcgaggcatgc 2078 Title: Perfect score: Sequence:

Scoring table:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

4109280 Total number of hits satisfying chosen parameters:

2054640 seqs, 14551402878 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:* Database :

gb_ba:* gb_htg:* em_fun:* gb_vi:* em_ba:* gb_pat:* b_sts: gb_ph:* gb_p1:* gb_pr:* em_hum: اp_un: م gb_om: b_ro gb_ov:

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

PAT 30-MAY-2001

linear

DNA

Sequence 2 from Patent EP1085089.
AX139462
AX139462.1 GI:14275107 human. RESULT 1 AX139462 LOCUS DEFINITION ORGANISM ACCESSION VERSION KEYWORDS SOURCE

Homo sapiens
Busaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2078)
1 (bases 1 to 2078)
1 Hombar Cyclic nucleotide phosphodiesterase
Human Cyclic nucleotide phosphodiesterase
Patent: EP 1085089-A 2 21-MAR-2001;

REFERENCE AUTHORS TITLE JOURNAL

N N N	- G 5	01 AGGCTTTTGTCATCTTTGTGGACTTGGCATCAACAACAACAATTATGTATG
/organism="homo sapiens" /db_xref="taxon:9606" 5 a 439 c 491 g 533 t	oy oy	1 AGAAGTCCTGGGCCAAGCAGTCTGTGGCTCTTGATGTGTTCATACCATGCAACCAAGTTT 102
ch 11 Similarity 100.0%; Score 2078; DB 6; Length 2078; 2078; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	do Db	1 CAAAAGTTGACAAGTTTAAGGCAGCCAACATCCCTCTGGTGTCAGAACTTGCCA 108 
GGTCCGAGATGCTGAAGCGAGGAAGAACTTTATTCAGAAATGTGCTCAGTGCCCACAC 60 	Qy Db	81 TCGATGACATTCATTTTGATGACTTTTTCTCGAGGTTGATGCCATGATCACAGCTGCTC 114
AGTGGAAAAAGGTGAAAATCACAAGGTGGTCCAAATCTCTGGGGCCTCTTTGGCTGAAA 120 	yo da	1141 TCCGGATGTTCATGGAGCTGGGATGGTACAGAAATTTAAAATTGACTATGAGACACTGT 1200 
CGAT 18	Qy Op	1201 GTAGGTGGCTTTTGACAGTGAGGAAAACTATCGGATGGTTCTATACCACAACTGGAGAC 1260 
CCTA 24	oy da	1261 ATGCCTTCAACGTGTCAGCTGATGTTCGCGATGTTAACCACTGCTGGGTTTCAAGACA 1320 
GAAG 30	da .	21 TTCTGACCGAGGTGGAAATTTAGCGGTGATTGTGGGATGCCTGTGTCATGACCTCGACC 138 11111111111111111111111111111111111
GAGCTCCATTTACTGAAGATGATGAAAAGTTATGCAGATGTATCTTCCATTTTGTGGAA 360   -	oy Op	1381 ACAGGGAACCAACGATGCCTTCCAAGCTAAGAGTGGCTCTGCCCTGGCCCAACTCTATG 1440
AGAG 42	QY	rctgctaccttggagcatcaccatttcaaccacgcgtgatgatgct 
STCA 4	ov O	1501 AGGGTCACAATATCTTTGCTAACCTGTCCTCCAAGGAATATAGTGACCTTATGCAGCTTT 1560 
CTCC 54	Qy Dp	1561 TGAAGCAGTCAATATTGGCAACAGACCTCACGCTGTACTTTGAGAGGAGAACTGAATTCT 1620 
CCAA 60	Qy Op	1621 TTGAACTTGTCAGTAAAGGAGAATACGATTGGAACATCAAAAACCATCGTGATATTTC 1680 
TCCG	Qy	1681 GATCAATGTTAATGACAGCCTGTAGAGCCGTGACCAACCGTGGGGGACATCTCCA 1740,
AACA 7	δλ Dp	1741 GACAGGTGGCAGAACTTGTAACCAGTGAGTTCTTCGAACAAGGAGATCGGGAGAGATAG 1800 
TTTC 78	QQ DP	1801 AGCTCAAACTCACTCAGCAATTTTGATCGGAACCGGAAGGATGAACTGCCTCGGT 1860 
AGALCTGTTCTTGTGTCCCTATTTGGAATAGCAACCACCAAATAATTGGAGTGG 84 ALH	. Qy Db	1861 TGCAACTGGAGTGGATTGATAGCATCTGCATGCCTTTGTATCAGGCACTGGTGAAGGTCA 1920 
11116 90 11111 00 001111111111111111111111111	. Oy	1921 ACGTGAAACTGAAGCCGATGCTAGATTCAGTAGCTACAAACAGAAGTAAGT
GTGA 96	Oy	1981 TACACCAAAAACGACTGCTGACTGACTGCTCATCCTCCTCCTGCCAGTGTTATGG 2040

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WLINNSIAELVASTGLPVNISDAYQDPRFDAEADQISGFHIRSVLCVPIWNSNHQIIG
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ATCSRAEVDRFRAANIPLLSELAIDDIHFDDFSLDDDAMITAALEMPREMELGWVGKFKI
DYETLCRWLLTVRKRWIVLHWRHAFNVCQLMFAALTAALEMPREGWVGKFKI
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EKS DLMQLLLAGSILATVFERFEFELYSKGFYDWNTKNHRDIFSKALMYACD
IGAVTKFWEISRQVARELVTSFFFFEGGORFERLEIKLTPSAIFPRALMYACD
IGAVTKFWEISRQVARELVTSFFFEGGORFERLEIKLTPSAIFPRALMYACD
SICMPLYQALVWRVIKFMILDSVATNRSKWEELHQKRLLASTASSSSPASVWAKED
1981 TACACCAAAAACGACTGCTGGCCTCAACTGCCTCCTCCTCCCCCGCCAGTGTTATGG 2040
                                                                                                                                 A linear PRI 09-NOV-2000 nucleotide phosphodiesterase
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Hetmon,J.M., Robas,N., Baxendale,R., Fidock,M., Phillips,S.C., Soderling,S.H. and Beavo,J.A.
Cloning and characterization of two splice variants of human
                                                                                                                              HSA278682 2502 bp mRNA linear PRI 09-NOV-20 HOmo sapiens mRNA for cAMP/CGMP cyclic nucleotide phosphodiestera AJZ78682 AJZ78682. GI:11136968 cAMP/CGMP cyclic nucleotide phosphodiesterase 11A3; PDE11A3 gene.
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Ramsgate Road, Sandwich,
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/codon_start=1
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                                           2041 TAGCCAAGGAAGACAGGAACTAATAACTCGAGGCATGC
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                             2041 TAGCCAAGGAAGACAGGAACTAATAACTCGAGGCATGC
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Submitted (19-JUL-2000) Robas N.M.,
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1. .2502
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/gene="PDE11A3"
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/gene="PDE11A3"
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Matches 2058; Conservative
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AAAAAGGTGAAAATCACAAGACTGGTCCAAATCTCTGGGGCCTCTTTGGCTGAAAAACAG
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Euteleostomi;

phosphodiesterase

Sasaki, T.

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/product...phosphodiesterase 11A2"
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CLCHDLDHRGTNNAFQAKSGSALAQLYGTSATLEHHHFNHAVMILQSEGHNIFANLSS
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LGAVTKPWEISRQVAELVTSEFFEQGDRERLELKLTPSAIFDRNRKDELPRLQLEWID
SICMPLYQALVKVNVKLKPMLDSVATNRSKWEELHQKRLLASTASSSSPASVWVAKED
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                                                                                                                                                                         Yuasa K. and Omori, K. Diract Submission (07-FBB-2000) Kenji Omori, Tanabe Seiyaku Co. Ltd., Discovery Research Laboratory; 2-50 Kawagishi-2-chome, Toda, Saitama 335-8505, Japan (E-mail:K-omori@tanabe.co.jp, Tel:+81-48-433-8069, Fax:+81-48-433-8159)
                                            Catarrhini; Hominidae;
                                Vertebrata;
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                                                                        Michibata, H.,
                                                                                                    characterization of two novel p
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                              Craniata;
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Pred. No. 0;
0; Mismatches
                                                                        luasa, K., Kotera, J., Fujishige, K.,
                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens'
/db_xref="taxon:9606"
/tissue_type="testis"
1. .3507
 to mRNA
                              Chordata;
                                            Primates;
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                                                                                                                   PDE11A variants showing
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sapiens testis sapiens
                              Eukaryota; Metazoa;
Mammalia; Eutheria;
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Best Local Similarity 100.
Matches 2057; Conservative
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                                                                                       Omori, K.
Isolation and
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/protein_id="AAG32023.1"
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Hetman,J.M., Robas,N., Baxendale,R., Fidock,M.,
Soderling,S.H. and Beavo,J.A.
Cloning characterization of two splice varian
phosphodiesterase 11A
Proc. Natl. Acad. Sci. U.S.A. 97 (23), 12891-128
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Hetman, J.M., Soderling, S.H. and Beavo, J.
Direct Submission
Submitted (23-JUN-2200) Pharmacology, Un
1959 NE Pacific St., Seattle, WA 98195,
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Direct Submission
Submitted (04-APR-2001) Kenji Omori, Tanabe Seiyaku Co. Ltd.,
Discovery Research Laboratory; 2-2-50 Kawagishi, Toda, Saitama 335-8505, Japan (E-mail:k-omori@tanabe.co.jp, Tel:81-48-433-8068, Pax:81-48-433-8159)
                  AGCTAAGAGTGGCTCTGCCCTGGCCCAACTCTATGGAACCTCTGCTACCTTGGAGCATCA
                                                  CCATTTCAACCACGCCGTGATGATCCTTCAAAGTGAGGGTCACAATATCTTTGCTAACCT
                                                             GTCCTCCAAGGAATATAGTGACCTTATGCAGCTTTTGAAGCAGTCAATATTGGCAACAGA
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Rattus norvegicus RNPDE11A3 mRNA for phosphodiesterase 11A3,
COMPLETE CGS.
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/translation="MIKORRESFRNVRSATOWRKVOSTROGOISGAFLAERLDKHOD FLTRANGTRFRDRENDELDKLTGYKTKSLLCMPIRNSDGEIIGVAQAINKVPEGAPFT EDDEKVWOMYLPFGEGIALSNAOLFAASKREFBRSRALLEVNNDLFEGETDLEKTVKKI EDDEKVWOMYLPFGEGIALSNAOLFAASKRESFELMSPKCSADAENSFRESVEKSYSTE MHAAOTLLKCERCSVLLLEDIESPVWFTKSFELMSPKCSADAENSFRESVEKSSYSD WLINNSIAELOYGSVLLLEDIESPVFTFGGIANTITYDOWKSWASWOSVADIGG VAQVITANLGKFFADADORLFERAFVTFGGICTNNTITYDOWKSWASWOSVADIOLSKY ACGSKAEVDKFKAANIPLYSELAIDIHFDDFSLDVDAMITAALRMFMELGWYGFKI DYETLCRWLLTVRKNYRWVLYHNWRHAFNVCQLMFAMITTAGFGEILTRVING CLCHDLDHGGILWFDFSLDVDAMITAALRMFMELGWYGFKI DYETLCRWLLKOSILATDLTLYFRRNYFRYNLSSKOCHHAWNYNIGGEGHNFANLSSKYSDLMOLLKGSILATDLTLYFRRNTHERFELUSKGAYDMSITSHROFFSNLMTAGCD LGAVTKPWELSRQVARLYSEFFEQGORERSELKTPSAIFDRNNKDELPRLQLEMID SICMPLYQALVKUNAKLKPMLDSVAANRRKWEELHQKRLQVSAASPVPSSSPSPAVAGE
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/protein_id="BAB79628.1"
/db_xref="GI:18143351"
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/organism="Rattus
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TSLSYKILIFYCLMVDADRCSLFLVEGAAAGKKTLVSKFFDVHAGTPLLPCSTTENSN
ETGVPWGKGITGYVGEHGETVNIPDAYQDRRFNDEIDKLTGYKTKSLLCMPTRNSDGE
ILGVAQAINKYPEGAAPFTEDDEKVMQMYLDATISNAQLFAASRKEYERSRELLEV
VNDLFEEQYDLERIYKKIMHRAQTLLKCERCSYLLLEDIESPVVKFRSFELMSPKCS
ADAENSFKESVEKSSYSDWLINNSIAELVASTGLPVNVSDAYQDPRFDAEADQISGFH
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/db_xref="G1:18143359"
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/db_xref="G1:1814359"
/db_xref=
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                 Yuasa,K., Ohgaru,T., Asahina,M. and Omori,K.
Identification of rat cyclic nucleotide phosphodiesterase 11A
(PDE11A): comparison of rat and human PDE11A splicing variants
Eur. J. Blochem. 268 (16), 4440-4448 (2001)
                                                                                          AAACTCACTCCTTCAGCAATTTTTGATCGGAACCGGAAGGATGAACTGCCTCGGTTGCAA
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Yuasa, K. and Omori, K.
Direct Submission
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                                                                                                                                                                  TTGTGGACTTGGCATCAACAACAACTTATGTATGATCAAGTGAAGAAGTCCTGGGCCAA
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                                                                ACTTGATGGGAAACCTTTTGATGATGCAGATCAACGACTTTTTGAGGCTTTTTGTCATCTT
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YHWRHARPWVCQLMPAMITAAGFODILTEVETLAVIYGGCCEGHLDHRGYNBROAKSG
SALAQLYGTSATLEHHFNHATWAILQSEGHNIFANLSSKEYSDLWQLLKQSILATDLI
LYFERRTEFFELVSKGEYDWNIKHRDIFRSMLMTACOLGAYTKPWELSKQYBLLYD
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                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 1784)

Fawcett,L., Baxendale,R., Stacey,P., McGrouther,C., Harrow,I., Soderling,S., Hetman,J., Beavo,J.A. and Phillips,S.C. Molecular cloning and characterization of a distinct human. Phoc. Natl. Acad. Sci. U.S.A. 97 (7), 3702-3707 (2000)
                                                                                                                                                                                                                                                                    Pfizer
UNITED
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           nucleotide phosphodiesterase 11A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="cyclic nucleotide phosphodiesterase 11A1"
/protein_id="CAB82573.1"
/db_xref="G1:7327961"
                                                                                                                                                                                                                   2 (bases 1 to 1784)
Phillips,S.C.
Direct Submission
Submitted (20-DEC-1999) Phillips S.C., Discovery Biology,
Central Research, Ramsgate Road, Sandwich, Kent CT13 9NJ,
KINGDOM
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                                   AJ251509.
AJ251509.1 G1:7327960
Cyclic nucleotide phosphodiesterase 11A1; PDE11A gene
Homo sapiens.
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/clone_lib="lambda-gt10"
/dev_stage="adult"
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/db_xref="taxon:9606"
/clone="lambda-la.1"
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           Homo sapiens mRNA for cyclic (PDE11A gene).
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/gene="PDE11A"
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TITLE Direct Submission JOURNAL Submitted (14-FEB-2002) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:Ghnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416) COMMENT NEDO human cDNA Sequencing project supported by Ministry of Economy, Trade and Industry of Japan: CDNA full insert sequencing:	(	Source 12003 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="HEB10314" /cell_line="Heb62"		tch al Similarity 99.8%; Pred. No	Matches 1019;         Conservative         0;         Mismatches         1;         Indels         1;         Gaps           1044         AAGGCAGCCAACATCCCTCTGGTGTCAGAACTTGCATCGATGACATTCATT	Db 1 AAGGCAGCCAACATCCTTGGTGTCAGAACTTGCCATGACATTTTGATGAC 60 Qy 1104 TTTTCTCTGACGTTGATGCCATGATCACAGCTGCTCTCCGGATGTTCATGGACTGGG 1163	Db 61 TTTCTCTCGACGTTGATGCCATGATCACAGCTGCTCTCCGGATGTTCATGGAGCTGGGG 120 Oy 1164 ATGGTACAGAAATTTAAAATTGACTATGAGACACTGTGTAGGTGTAGGTGTAGACAGTAGACAGTGAGG 1223	121		Qy 1284 ATGTTCGCGATGTTAACCACTGCTGGTTCAAGACATTCTGACCGAGGTGGAAATTTTA 1343	Qy 1344 GCGGTGATTGTGGGATGCCTGTGTCATGACCTCGACCAGGGGAACCAACAATGCCTTC 1403	Qy 1404 CAAGCTAAGAGTGCTCTGGCCCAACTCTATGGAACCTCTGCTACCTTGGAGCAT 1463	Qy 1464 CACCATTTCAACCACGCGTGATGATCTTCAAAGTGAGGGTCACAATATCTTTGCTAAC 1523 11	QY 1524 CTGTCCTCCAAGGAATATAGTGACCTTATGCAGCTTTTGAAGCAGTCAATATTGGCAACA 1583	Qy 1584 GACCTCACGCTGTACTTTGAGAGGAGAACTGAATTCTTTGAACTTGTCAGTAAAGGAGAA 1643	Oy 1644 TA-CGATIGGAACAICAAAAACCAICGIGAIATATTICGAICAAIGTTAAIGACAGCCTG 1702
1188	1308 TTTAACCAGGGGGGAGATGATCATCAGAGGGTCACAACATCTTGCTAATTGTCC 1367 1530 TCCAAGGAATATAGTGACCTTATGCAGCTTTTGAAGCAGTCAATATTGGCAACAGACCT 1589 11111111111111111111111111111111111	ACGCTCTACTTTGAGAGGAGAACTGAATTCTTTGAACTTGTCAGTAAAGGAGAATACGAT 	1650 TGGAACATCAAAACCATGTGATATTTTGATCAATGTTAATGACAGCCTGTGACCTT 1709 	GGAGCCGTGACCAAACCGTGGGAGATCTCCAGACAGGTGGCAGAACTTGTAACCAGTGAG 176 [	TTCTTCGAACAAGAGAATCGGGAGAATTACAGCTCAAACTCACTC	1830 GAILGGAACGGAAGGAIGAACTIGCGATIGCAATIGGAGTIGGATIGGA	1890 ATGCTTTGTATCAGGCACTGGTGAAGGTCAACGTGAAGCTGAAGCCGATGCTAGATTCA 1949 	1950 GTAGCTACAAAAGTAAGTGGGAAGACCTACACCAAAAACGACTGCTGGCCTCAACT 2009 	GCCTCATCCTCCTCCCTGCCAGTGTTATGGTAGCCAAGGAAGACAGGAACTAATAA 2	1846 GCCTCCCCAGTCCCTTCCAGTCCCAGCGGTGGCCGGAGAGGACAGACTGTAAACC 1907 2067 CTCGAGGCATGC 2078 	1908 ACCCAGAGCTGC 1919	ARO74273 AKO74273 2083 bp mRNA linear PRI 15-FEB-2002 DEFINITION Homo sapiens CDNA FLJ23693 fis, clone HEP10314, highly similar to Home sapiens mbNa for outly managed to sapiens with the sapiens when the sapiens when the sapiens were sapiens with the sapiens when the sapiens when the sapiens were sapiens when the sapiens when the sapiens when the sapiens were sapiens when the sapiens when the sapiens were sapiens were sapiens which were sapiens which were sapiens which were sapiens when the sapiens were sapiens were sapiens which were sapiens when the sapiens were sapiens were sapiens which were sapiens which were sapiens which were sapiens when the sapiens were sapiens were sapiens which were sapients whill w	ACCESSION AK074273  VERSION AK074273.1 GI:18676819  KEYWORDS Oligo capping; fis (full insert sequence).  SOURCE Homo sapiens hepatoma cell_line:HepG2 cDNA to mRNA, clone lib:HEP	st	Hikiji,T., Kobata Okitani,R., Ota,T.	TITLE SILBARIATIONA SEQUENCING Project JOURNAL Unpublished REFERENCE 2 (bases 1 to 2083) AUTHORS Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T., Shibahara,T., Tanaka,T. and Nakamura,Y.

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PTHANGQTSSSRGGSGATTPVRKISAHEFERGGLLKPIVNTIDGTPTFLSIGPPMDNG
SVGGSCSNLQNVGGVVAGOYQYNHQQHHHNHAHLHHSQHSHYQAGGAVGSSSLGSTGG
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HYQPLNHSGAAPPSSSNGSSSGGGVQTSATPQQQQQYQVQQDYQYQYQHYYHHQANS
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SGDVTGVAQVINKMNGECFSIIDERVYSSYLDGFOGTGLIANAQLYKESQLEJRKNUVL
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SEEEATSRTSPYESRPPINIGITGHVATTGETVNVPNAYEDDRFDASVDENSCFKHRS
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AMAKQSVTLEVLSYHASATMDEAHRLRRLRVPSAVHFRLHDFKFDDIHFEDDDTLKAC
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LEVRTLCHKILQNVSILLNADRGSLFLVQGRCNGPDGLKKCLVSKLFDVCPRSTVEEM
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LNSPGNQILANLSSDDYCRVIRVLEDAILSTDLAVYFKKRGPFLESVSQPTSYWVAEE
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HHHHHHSHHNHSQHGTGIGSARIGGSGLISLTTPLLANDSDRIPKIVGKIGNLDGLPF
ANGIGGPQNGHGLPFGSYGHHHHQHHHHLLARRHSETNSNGATAMAVEK"
1445 c 1399 g 1218 t
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                                                                                                                                                                                                                                                                                                                                                                      /translation="MKVTQSEENTRNTSDRSKSVQTNRKFDNFNWLLSCGLLAAVKST
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                                                                                                                                                                                                                                                                                                                                          /db_xref="FLYBASE:FBgn0032686"
                                                                                           /db_xref="FLYBASE:FBgn0032686"
                                                                                                                                                                                                                                                                        /protein_id="AAM52774.1"
/db_xref="G1:21483598"
      'db_xref="taxon:7227"
                                                                                                                                                                                   /note="Longest ORF"
                                                                                                                                                                                                                                               /product="SD13096p"
                                                                                                                                                   /gene="CG10231"
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1 (bases 1 to 5687)

Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
Champe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E.,
George, R., Gonzalez, M., Guarin, H., Kronmiller, B., Li, P., Liao, G.,
Miranda, A., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S.,
Patel, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M.
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This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal
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CATCTGCATGCCTTTGTATCAGGCACTGGTGAAGGTCAACGTGAAACTGAAGCCGATGCT
                                                                                                                                                                                                                                                                                                                                                                      AGATTCAGTAGCTACAAACAGAAGTAGGGAAGAGCTACACCAAAAACGACTGCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (14-JUN-2002) Berkeley Drosophila Genome Project, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, USA Sequence submitted by:

Berkeley Drosophila Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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SD13096 full insert cDNA.
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ORGANISM

SOURCE

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

DEFINITION

ACCESSION VERSION KEYWORDS

RESULT 11

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FEATURES

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589 TGATGTCCCCAAAGTGCAGTGCTGAGAACAGTTTCAAAGAAAG	TATCTGGTTTTCACATAGATCTTTTTTTTTTTTTTTTTT	ATGATCAAGTGAAGAAGTCCTGGGCCAAGCAGTTGTGGCTTTGATGTGCTGTTGATGTGTGTG		GGTTTCAAGACATCTGACCGAGGTGGAATTTTAGCGGTGATTGTGGGATGCCTGTGCC  GGTTTCAAGACATCTGACCGAGGTGGAATTTTAGCGGTGATTGTGGGATGCCTGTGC  ATGACCTCGACCACGAGAATCGTTGGCGTTATTTTTTTTT	CCCAACTCTAIGGAACCTCGCTACCTGGACCATCACCATTICACCCCTTGGACCACCACCACCACCACGCGGTGATGA  [	GAGGA 160 

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C12N15/09,C07K16/40,C12N1/21,C12N9/16,C12Q1/34//A61K38/46, PC
169 AGGATCGACGATTCAATGATGAAATCGACAAGCTGACTGGATACAAGACAAAATCATTAT
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Tarui,N., Tsuchiya,T. and Nakahama,K. Novel protein and DNA thereof
Patent: JP 2000354492-A 6 26-DEC-2000;
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/organism='Homo sapi
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/db_xref="taxon:9606"
412 c 484 g 588
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JP 2000354492-A/6
26-DEC-2000
19-JUL-1999 JP 1999204336
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OS HOMO Sapiens (hur
PD 26-DEC-2003
PF 19-JUL-1999 JP 19
PR NAOKI TARUI,TAKA)
PC CL2N15/09,CO7K16,
A61K88/55,
PC A61K8/754,A61K37,
PC A61K37/54,A61K37,
PC A6
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CGCGATGTTAACCACTGCTGGGTTTCAAGACATTCTGACCGAGGTGGAAATTTTAGCGGT
           GATTGTGGGATGCCTGTGTCATGACCTCGACCACGGGGAACCAACAATGCCTTCCAAGC
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Francis,S.H., Loughney,K., Beavo,J.A., Corbin,J.D., Kadlec
Ferguson,K.M., Mcallister-Lucas,L.M., Sonnenburg,W.K. and
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                                                                                                                                                                                          SHLDVTALCHKIFLHIHGLISADRYSLFLVCEDSSNDKFLISRLFDVAEGSTLEEVSN
NCIRLEWNKGIVGHVAALGEPLNIKDAYEDPRFNAEVDQITGYKTQSILCMPIKNHRE
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TEAVBRAMARONVTLEVLSYRASABEETRELOGASAAAVVPSAQTLKTTDFSFEDFEL
SDLETALCTTRAFTDLLVQNKDMKEPVLCMXLSVKRNYRNNYRHWRHAFNTAO
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HHPPDQCLMTINSPGNOILSGLSIEBKYTTLKTTROATLAFDLALYTKRGEFFELIR
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DLASLIFEEQQSLEVILKKIAATIISFMQVQKCTIFIVDEDCSDSFSSVFHMECEELE
KSSDTLTREHDANKINYMYAQYVKNTMEPLNIPDVSKDKRFPWTTENTGNVNQQCIRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1231 TCAATTACATGTATGCTCAGTATGTCAAAAATACTATGGAACCACTTAATATCCCAGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGATCGACGATTCAATGATGAAATCGACAAGCTGACTGGATACAAGACAAAATCATTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGATTCCTG---AAGGAGCTCCATTTACTGAAGATGAAAAAAGTTATGCAGATGTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTCCATTTTGTGGAATCGCCATATCTAACGCTCAGCTCTTTGCTGCCTCAAGGAAAGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTTCTGTTTTACTCCTAGAGGACATCGAATCACCAGTGGTGAAATTTACCAAAATCCTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 356.6; DB 6; Length 2645;
Pred. No. 2e-86;
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protein product"
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TTTGCCAACTTGTTAATAAGATGGAGGAGAATACTGGCAAGGT	GCAGATCAACGACTTTTGAGGCTTTTGTCATCTTTTGTGGACT		AATTATGTATGATCAAGTGAAGAAGTCCTGGGCCAAGCAGTGTGGCGTTTGATGTGTGT	CAGATGTATGAAGCAGTGGAGAGCCATGGCCAAGCAAATGGT	ATCATACCATGCAACATGTTCAAAAGCTGAAGTTGACAAGTTTAAGGCAGCCAACATCCC 	TCTCGTGTCAGAACTTGCCATCGATGACATTCATTTTGATGACTTTTCTCT	GTGGTGCCATCTGCCCAGACCCTTAAAATTACTGACTTTAGCTT	CGACGTTGATGCCATGATCACAGCTGCTCCGGATGTTCATGGAGCTGGGGATGGTACA	GAAATTTAAAATTGACTATGAGACACTGTGTAGGTGGCTTTTGACAGTGAGGAAAAACTA	AACTTCCAGATGAACATGAGGTTCTTTGCAGATGGATTTTAAG:	TCGGATGGTTCTATACCACAACTGGAGACATGCCTTCAACGTGTGTCACCTGATGTTT	CGCGATGTTAACCACTGCTGGGTTTCAAGACATTCTGACCGAGGTGGAATTTTAGCGGT	GCTGCTCTAAAAGCAGCAAAATTCAGAACAAGCTGACCT	GATTGTGGGATGCCTGTGTCATGACCTCGACCAGGGGAACCAACAATGCCTTCCAAGC	CIGATIGCTGCACTAAGCCACGATTTGGATCACCGTGTGTAAA	TAACAGTGGCTCTGGCCCAACTCTATGGAACCTCTGCTACCTTGGAGCATCACCA	CGAAGTGAACATCCACTTGCCCAGCTTTACTGCCATTCAAT(	TTTCAACCACGCCGTGATGATCCTTCAAAGTGAGGGTCACAATATCTTTGCTAACCTGTC	CTCCAAGGAATATAGTGACCTTATGCAGCTTTTGAAGCAGTCAAT/		CACGCTGTACTTTGAGAGGAGAACTGAATTCTTTGAACTTGTCAGTAAAGGAGAATACGA	AGCACTGTACATTAAGAGGCGAGGAGAATTTTTTGAACTTATAAG	TIGGAACATCAAAAACCATGGTATATTTGGATCAATGTTAATGACAGCCTGTGACCT	** ジャンシーシン・ジャン・シー・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・	TCTGCAATTACAAAACCCTGGCCTATTCAACAACGGATAGCAGAACTTGTAGCAACTGA	:TTCTTCGAACAAGGAGATCGGGAGAGATTAGAGCTCAAACTCAC		TGATCGGAACCGGAAGGATGAACTGCCTCGGTTGCAACTGGAGTGGATTGATAGCATCTG	AACAGGGAGAAGAAAACAAAATCCCAAGTATGCAAGTTGGGTT	CATGCCTTTGTATCAGGCACTGGAAGGTCAACGTGAAACTGAAGCCGATGCTAGATTC	TTGCAACTGTATGAGGCCCTGACCCÁCGTGTCAGAGGACTGTTT
1411 T	881 T	1469 A	941 A	1529 G	1001 A	H - E	σ	1112 C 1709 G	1172 G	1769 G	1232 T   1829 T	1289 C	1889 T	1349 G	1949 G	60	2009 G	1469 T 2066 T	σ	26	1589 0	2186 A	1649 T 2246 T	6	90	1769 G	2366 A	1829 I	2426 G	1889 C	2486 0
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